

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 05:13:50 ; Search time 3743 Seconds

(without alignments)

18002.148 Million cell updates/sec

US-10-083-853B-2

Perfect Score: 29921

Sequence: 1 gttatgtagaagacgtca.....caattctgtgaagaaagtaa 29921

Scoring table: OLIIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: N Geneseq_101002.*

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	652	2	1587	22	AAS04493 Human FCTR2 DNA pr
C 2	652	2	1728	22	AAS04498 Human PGDF DNA.
C 3	652	2	1828	22	AAS04492 Human FCTR1 DNA pr
C 4	652	2	3718	24	AAD25489 Human LP85 DNA #2.
C 5	652	2	3736	24	AAD25488 Human LP85 DNA #1.
C 6	601	2	1934	21	AAD00737 Human Platelet Der
C 7	601	2	2253	21	AAD00738 Human Platelet Der
C 8	601	2	3798	22	AAS046939 Human secreted pro
C 9	601	2	4001	22	AAS046957 Human secreted pro

10	499	1.7	2726	22	AAS046959 Human secreted pro
11	460	1.5	485	24	ABL63632 Breast cancer rela
C 12	377	1.3	1882	21	AAC81555 Human growth facto
C 13	377	1.3	1882	21	AAS1541 SEQ. ID. 36 from W
C 14	377	1.3	1882	22	AAS47772 Human zveg4 polyp
C 15	377	1.3	1882	24	ABQ73239 Human zveg4 encod
C 16	377	1.3	3853	22	AAF24196 Human VEGF-G cDNA.
C 17	221	0.7	620	22	ABA08941 Human novel protei
C 18	221	0.7	1110	22	AAF24197 Human VEGF-G codin
C 19	221	0.7	1162	22	AAS21336 Human cDNA sequenc
C 20	221	0.7	1162	24	ABL55717 Human angiogenesis
C 21	221	0.7	1162	24	ABL88228 Human PR04345 cDNA
C 22	221	0.7	1404	24	AAD25490 Human LP85 DNA #3.
C 23	220	0.6	462	22	AAS04496 Human FCTR5 DNA pr
C 24	185	0.6	360	21	AAD00739 Human Platelet Der
C 25	165	0.6	690	21	AAD00736 Human Platelet Der
C 26	155	0.5	2057	23	AAS73168 DNA encoding novel
C 27	155	0.5	2253	23	AAS73143 DNA encoding novel
C 28	155	0.5	2480	23	AAS69375 DNA encoding novel
C 29	155	0.5	2558	22	ABA15787 Human nervous syst
C 30	155	0.5	3303	23	AAS78786 DNA encoding novel
C 31	155	0.5	3303	23	AAS91891 DNA encoding novel
C 32	155	0.5	3309	23	AAS72051 DNA encoding novel
C 33	155	0.5	3309	23	AAS78174 DNA encoding novel
C 34	155	0.5	3309	23	AAS78439 DNA encoding novel
C 35	155	0.5	3573	23	AAS69829 DNA encoding novel
C 36	155	0.5	3573	23	AAS70806 DNA encoding novel
C 37	155	0.5	3573	23	AAS87857 DNA encoding novel
C 38	155	0.5	3573	23	AAS92380 DNA encoding novel
C 39	155	0.5	3890	22	AAS27695 DNA encoding novel
C 40	155	0.5	3890	23	ABK42841 Genomic sequence #
C 41	155	0.5	3915	23	AAS78976 DNA encoding novel
C 42	155	0.5	3922	22	AA198916 Human excretory re
C 43	155	0.5	3922	22	AAS30399 DNA encoding novel
C 44	155	0.5	3922	22	AA104426 Human reproductive
C 45	155	0.5	3922	22	AA163266 Human kidney relat

ALIGNMENTS

RESULT 1

AAS04493/C

ID AAS04493 standard; DNA; 1587 BP

XX AAS04493;

XX 07-SEP-2001 (first entry)

DT Human FCTR2 DNA present in clone 30664188.0.331.

XX Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; Graft versus host disease; coagulation; ds;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 540..938

FT /*tag= a /product= "Human" FCTR2"

XX

XX

XX

XX

XX

XX

XX 06-OCT-2000; 2000WO-US27671.

PF

XX PF 06-OCT-2000; 2000MO-US27671.
 XX PR 07-OCT-1999; 99US-0158083.
 XX PR 13-OCT-1999; 99US-0159231.
 XX PR 04-JAN-2000; 2000US-0174485.
 XX PR 03-MAR-2000; 2000US-0186707.
 XX PR 10-MAR-2000; 2000US-0188250.
 XX PR 08-AUG-2000; 2000US-0223879.
 XX PR 12-SEP-2000; 2000US-0662783.
 XX PR 20-SEP-2000; 2000US-0234082.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
 XX PI Jeffers M;
 XX DR WPI; 2001-316172/33.
 XX DR P-PSDB; AAU00704.
 XX Novel growth factor polypeptides termed as FCTR polypeptides, useful
 XX for treating cancer, cardiovascular and fibrotic diseases, diabetic
 XX ulcers, wound healing and neuronal disorders
 XX Disclosure; Fig 13; 171pp; English.
 XX The sequence represents DNA encoding a protein related to bone
 XX morphogenetic protein-1 (BMP-1), vascular endothelial growth factor
 XX (VEGF-E) and platelet derived growth factor (PDGF). Polypeptides and
 XX polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as
 XX FCTR polypeptides and nucleic acids. FCTR proteins are useful for treating
 XX or preventing a disorder associated with aberrant expression, aberrant
 XX processing, or aberrant physiological interactions of the proteins in a
 XX mammal, where the disorder is characterized by insufficient or
 XX ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia.
 XX The peptides and their associated nucleic acids are useful for both
 XX promoting and inhibiting growth of cells and tissues and in treatment of
 XX cancer, anaemia, leukopenia, baldness, for treating cardiovascular and
 XX fibrotic disorders, diabetic ulcers, obesity, infectious diseases,
 XX hyperproliferative and dysproliferative disorders, neurodegenerative
 XX disorders, osteoarthritis, inflammatory disorders, Graft versus host
 XX disease, coagulation disorders such as haemophilia, and neural disorders
 XX including Parkinson's disease, Alzheimer's disease, multiple sclerosis,
 XX Huntington's disease, amyotrophic lateral sclerosis, peripheral
 XX neuropathy, acute brain injury and epilepsy.
 XX SQ Sequence 1728 BP; 530 A; 364 C; 379 G; 455 T; 0 other;
 Query Match 2.2%; Score 652; DB 22; Length 1728;
 Best Local Similarity 100.0%; Pred. No. 1.9e-188;
 Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTATATGTAGAAGCCTCATCTTTTGATTTTAAATATACAAAGTCTTCTTTAAGAGA 60
 DB 1718 GTATATGTAGAAGCCTCATCTTTTGATTTTAAATATACAAAGTCTTCTTTAAGAGA 1659
 QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATAATATATCTCTAAATTTT 120
 DB 1658 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATAATATATCTCTAAATTTT 1599
 QY 121 CTAAGACATGTTTTCATATATTTGACCATCCCTTTATTTGGCAAAGGATTTAAGAGTCT 180
 DB 1598 CTAAGACATGTTTTCATATATTTGACCATCCCTTTATTTGGCAAAGGATTTAAGAGTCT 1539
 QY 181 AACTCAACATATGTAGTCTCTGGTGTACCTGGTTATATATACCAAAAAAACAATTGTAT 240
 DB 1538 AACTCAACATATGTAGTCTCTGGTGTACCTGGTTATATATACCAAAAAAACAATTGTAT 1479
 QY 241 CTATATACATACATAGATGAATATATTTCTGCTGTTGTTGTGCATATATAAACCCTAAAC 300
 DB 1478 CTATATACATACATAGATGAATATATTTCTGCTGTTGTTGTGCATATATAAACCCTAAAC 1419
 QY 301 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC 360

DB 1418 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC 1359
 QY 361 TTGCCATGGCATTAAACAAAGGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATTG 420
 DB 1358 TTGCCATGGCATTAAACAAAGGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATTG 1299
 QY 421 CAGGCTAGTAGTAAGTTTGGTTGCTGTAGTAAAGGGTCTCTTATCTACCCCTCCTTAA 480
 DB 1298 CAGGCTAGTAGTAAGTTTGGTTGCTGTAGTAAAGGGTCTCTTATCTACCCCTCCTTAA 1239
 QY 481 ACTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGGTCTT 540
 DB 1238 ACTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGGTCTT 1179
 QY 541 GAGCTGCAGATACAATCACATCTTTCATGTTGATCCAACTGGATGTCACATAGAGCCATG 600
 DB 1178 GAGCTGCAGATACAATCACATCTTTCATGTTGATCCAACTGGATGTCACATAGAGCCATG 1119
 QY 601 GTCTTAGCTCTACCCCTCTCTTGTGATGTGGCCAGGCTCAAACTCTTAATACCT 652
 DB 1118 GTCTTAGCTCTACCCCTCTCTTGTGATGTGGCCAGGCTCAAACTCTTAATACCT 1067
 RESULT 3
 AAS04492/c
 ID AAS04492 standard; DNA; 1828 BP.
 XX AC AAS04492;
 XX DT 07-SEP-2001 (first entry)
 XX DE Human FCTR1 DNA present in clone 30664188.0.99.
 XX KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
 KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
 KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
 KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
 KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
 KW inflammatory disorder; Graft versus host disease; coagulation; ds;
 KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
 KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
 KW peripheral neuropathy; acute brain injury.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 182..1294
 FT /tag= a
 FT /product= "Human FCTR1"
 FT sig_peptide 182..250
 FT /tag= b
 FT mat_peptide 251..1291
 FT /tag= c
 FT /product= "Mature human FCTR1"
 XX WO2001125437-A2.
 XX PN 12-APR-2001.
 XX PD 06-OCT-2000; 2000MO-US27671.
 XX PF 07-OCT-1999; 99US-0158083.
 XX PR 13-OCT-1999; 99US-0159231.
 XX PR 04-JAN-2000; 2000US-0174485.
 XX PR 03-MAR-2000; 2000US-0186707.
 XX PR 10-MAR-2000; 2000US-0188250.
 XX PR 08-AUG-2000; 2000US-0223879.
 XX PR 12-SEP-2000; 2000US-0662783.
 XX PR 20-SEP-2000; 2000US-0234082.
 XX PA (CURA-) CURAGEN CORP.
 XX

PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX WPI: 2001-316172/33.
DR P-PSDB; AAU00698.
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful
PT for treating cancer, cardiovascular and fibrotic diseases, diabetic
PT ulcers, wound healing and neuronal disorders
XX
PS Claim 11; Page 11-12; 171pp; English.
XX
CC The sequence represents DNA encoding a protein related to bone
CC morphogenetic protein-1 (BMP-1), vascular endothelial growth factor
CC (VEGF-E) and platelet derived growth factor (PDGF). Polypeptides and
CC polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as
CC FCTR polypeptides and nucleic acids. FCTR proteins are useful for treating
CC or preventing a disorder associated with aberrant expression, aberrant
CC processing, or aberrant physiological interactions of the proteins in a
CC mammal, where the disorder is characterised by insufficient or
CC ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia.
CC The peptides and their associated nucleic acids are useful for both
CC promoting and inhibiting growth of cells and tissues and in treatment of
CC cancer, anaemia, leukopenia, baldness, for treating cardiovascular and
CC fibrotic disorders, diabetic ulcers, obesity, infectious diseases,
CC hyperproliferative and dysproliferative disorders, neurodegenerative
CC disorders, osteoarthritis, inflammatory disorders, Graft versus host
CC disease, coagulation disorders such as haemophilia, and neural disorders
CC including Parkinson's disease, Alzheimer's disease, multiple sclerosis,
CC Huntington's disease, amyotrophic lateral sclerosis, peripheral
CC neuropathy, acute brain injury and epilepsy.
XX
SQ Sequence 1828 BP; 572 A; 380 C; 385 G; 491 T; 0 other;
Query Match 2.2%; Score 652; DB 22; Length 1828;
Best Local Similarity 100.0%; Pred. No. 1.8e-188;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCTCATCTTTTGATTTTAAATATACAAAGATGCTTCTTTAAGAGA 60
DB 1818 GTATATGTAAGAAAGCCTCATCTTTTGATTTTAAATATACAAAGATGCTTCTTTAAGAGA 1759
QY 61 GCAAGATTCAAATTTGTTGTTTCAAAATTTTAAATTTTAAATTTTATCTCTAAATTTT 120
DB 1758 GCAAGATTCAAATTTGTTGTTTCAAAATTTTAAATTTTAAATTTTATCTCTAAATTTT 1699
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTGGCAAGAGTTTAAAGAGCT 180
DB 1698 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTGGCAAGAGTTTAAAGAGCT 1639
QY 181 AACTCAACATATGTAAGCTCTGGTGACCTGTTTATATATACCAAAAAACATTTGAT 240
DB 1638 AACTCAACATATGTAAGCTCTGGTGACCTGTTTATATATACCAAAAAACATTTGAT 1579
QY 241 CTAATACACATAGACATGAATATATTTCTGTGTGTTTGGCATATATAACCTCAAC 300
DB 1578 CTAATACACATAGACATGAATATATTTCTGTGTGTTTGGCATATATAACCTCAAC 1519
QY 301 ACTATATTAATGCAATCCTATATTTCTAGTATAGAGTTGATGATATACCTTTCTAC 360
DB 1518 ACTATATTAATGCAATCCTATATTTCTAGTATAGAGTTGATGATATACCTTTCTAC 1459
QY 361 TTGCCATGGCATTAAACAAAGGCTGAGACTCAGCAACACTTGTGTTGATTCATTCATG 420
DB 1458 TTGCCATGGCATTAAACAAAGGCTGAGACTCAGCAACACTTGTGTTGATTCATTCATG 1399
QY 421 CAGGCTAGTAGTAAGTTGGTTGGTGGTAGGAAAGGCTCTTATCTCACCCCTCTTAA 480
DB 1398 CAGGCTAGTAGTAAGTTGGTTGGTGGTAGGAAAGGCTCTTATCTCACCCCTCTTAA 1339
QY 481 ACTAAGCTTCTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGGTCTT 540
DB 1338 ACTAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGGTCTT 1279

QY 541 GAGCTGCAGATACAATACATCGTTTCATGGTGCATCCAACTGGATGTCAACTAGAGCATG 600
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QY 601 GTCCTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652
DB 1218 GTCCTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1167

RESULT 4
AAD25489/c
ID AAD25489 standard; DNA; 3718 BP.
XX
AC AAD25489;
DT 26-MAR-2002 (first entry)
XX
DE Human LP85 DNA #2.
XX
KW LP85; platelet-derived growth factor; PDGF; antinflammatory; vulnery;
KW osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;
KW MSD; therapy; bone growth; cartilage differentiation; wound healing;
KW neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
KW sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
KW muscle loss; immobility; bone density; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT sig_peptide 114..149
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FT mat_peptide 150..1205
FT /*tag= c
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XX WO200189450-A2.
PN 29-NOV-2001.
PD
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XX 08-MAY-2001; 2001WO-US11755.
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XX 19-MAY-2000; 2000US-205424P.
PR 11-JAN-2001; 2001US-261071P.
PR 11-JAN-2001; 2001US-261076P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;
PI Witcher DR, Wroblewski VJ;
XX
XX WPI: 200203040/11.
DR P-PSDB; AAEL5820.
XX
XX Analog of a platelet-derived growth factor homolog, LP85 useful for
PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
PT amino acid substitutions which destroy the tripeptidyl sequence of
PT native LP85
XX
XX Disclosure; Page 111-113; 117pp; English.
PS
XX
XX The present invention relates to LP85, an analogue of platelet-derived
CC growth factor (PDGF) homologue. Sequences of the invention are useful
CC for the manufacture of a medicament for treating musculoskeletal disorder
CC (MSD) which include promoting bone growth, cartilage differentiation and
CC function, wound healing, neuron growth, preventing cartilage degradation
CC or neuronal degeneration. They are useful for treating bone fractures,
CC osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,
CC tissue atrophy, traumatised connective tissues, grafted connective
CC tissues and/or transplanted organs, bone or muscle loss due to

CC	malignancy, endocrine disorders and immobility. They are also used
CC	for phylogenetically increasing or maintaining bone density in a
CC	mammal. The present sequence is a DNA encoding human LP85 protein.
XX	
XX	Sequence 3718 BP; 1157 A; 730 C; 715 G; 1116 T; 0 Other;
XX	
Query Match	2.2%; Score 652; DB 24; Length 3718;
Best Local Similarity	100.0%; Pred. No. 1.6e-188;
Matches 652; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB	1732 GTATATGTAAGAAGCCTCATCTTTTGATTTTAAATATACAAGATGCTTTCTTTAAGAGA 1673
QY	61 GCAAGATTCAAAATCTTTTGTCTTCCAAATTTAAAAATAAATTTATCTCCCTAAATTTT 120
DB	
DB	1672 GCAAGATTCAAAATCTTTTGTCTTCCAAATTTAAAAATAAATTTATCTCCCTAAATTTT 1613
QY	121 CTAAGACATGTTTCATATATATTGACATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 180
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DB	1612 CTAAGACATGTTTCATATATATTGACATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT 1553
QY	181 AACTCAAACATATGTAAGCTCTGGTCTGCTGCTGTATATATACCAAAAAAACAATTTGAT 240
DB	
DB	1552 AACTCAAACATATGTAAGCTCTGGTCTGCTGCTGTATATATACCAAAAAAACAATTTGAT 1493
QY	241 CTATATACATAGACATGAATATATTTCTGCTGTGTTGTGCATATATAAAGCTCAAC 300
DB	
DB	1492 CTATATACATAGACATGAATATATTTCTGCTGTGTTGTGCATATATAAAGCTCAAC 1433
QY	301 ACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC 360
DB	
DB	1432 ACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC 1373
QY	361 TTGCCATGCGATTAAACAAGCAAGCTGACACTCAGCAACCACTTGTTGTCATGCAATTG 420
DB	
DB	1372 TTGCCATGCGATTAAACAAGCAAGCTGACACTCAGCAACCACTTGTTGTCATGCAATTG 1313
QY	421 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAAGGTCTCTTATCTCACCTCCCTTAA 480
DB	
DB	1312 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAAGGTCTCTTATCTCACCTCCCTTAA 1253
QY	481 ACTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATTCCTTATCAGAGTGGTCTT 540
DB	
DB	1252 ACTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATTCCTTATCAGAGTGGTCTT 1193
QY	541 GAGCTCGACATACAATCACATCGTTTCATGTTGATGTCAGGCTCAAACTGTAATAGCT 600
DB	
DB	1192 GAGCTCGACATACAATCACATCGTTTCATGTTGATGTCAGGCTCAAACTGTAATAGCT 1133
QY	601 GTCTTAGCTTACCCCTCTCTTTGATGTGCCAGGCTCAAACTGTAATAGCT 652
DB	
DB	1132 GTCTTAGCTTACCCCTCTCTTTGATGTGCCAGGCTCAAACTGTAATAGCT 1081
RESULT 5	
AAD25488/C	
ID	AAD25488 standard; DNA; 3736 BP.
XX	
AC	AAD25488;
XX	
XX	26-MAR-2002 (first entry)
XX	
DE	Human LP85 DNA #1.
XX	
KW	LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnery;
KW	osteopathic; neuroprotective; tranquilizer; musculoskeletal disorder;
KW	MSD; therapy; bone growth; cartilage differentiation; wound healing;
KW	neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
KW	sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
KW	muscle loss; immobility; bone density; ds.
XX	
OS	Homo sapiens.


```
XX AC AAD00738;
XX KW Platelet Derived Growth Factor (PDGF)-D encoding complete cDNA.
XX DE 08-SEP-2000 (first entry)
XX DE Human Platelet Derived Growth Factor (PDGF)-D encoding complete cDNA.
XX KW Platelet Derived Growth Factor-D; PDGF-D; human; cytosolic; vulnary;
XX KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
XX KW proliferative; activator; proliferation; differentiation; motility;
XX KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
XX KW atherosclerosis; wound; metastasis; ss.
XX OS Homo sapiens.
XX PH Key
XX FT CDS
XX FT 176..1288
XX FT /tag= a
XX FT /product= "Human PDGF-D protein"
XX FT /note= "platelet derived growth factor"
XX PN WO200027879-A1
XX PD 18-MAY-2000.
XX PF 10-NOV-1999; 99WO-US26462.
XX PF 10-NOV-1999; 98US-0107852.
XX PR 28-DEC-1998; 98US-0113997.
XX PR 26-AUG-1999; 99US-0150604.
XX PR 04-OCT-1999; 99US-0157108.
XX PR 05-OCT-1999; 99US-0157756.
XX PA (LUDM-) LUDWIG INST CANCER RES.
XX PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
XX PI Oestman A, Heldin C;
XX WPI: 2000-376495/32.
XX P-PSDB: AAY71130.
XX Novel polynucleotides encoding a novel growth factor of cells
XX PT expressing a platelet-derived growth factor, useful for diagnostic and
XX PT therapeutic applications, e.g. concerning cancer -
XX PS Claim 1; Fig 7; 11pp; English.
XX CC The present sequence is the complete cDNA encoding human platelet derived
XX CC growth factor (PDGF)-D, formally known as Vascular Endothelial Growth
XX CC Factor (VEGF)-G. It is derived from human fetal lung lambda gt10 cDNA
XX CC library. It belongs to the VEGF/PDGF family. It functions as an activator
XX CC of proliferation, differentiation, growth and motility of cells, that
XX CC express PDGF-D receptor. This sequence is useful for inhibiting the
XX CC growth of tumours, that express PDGF-D. Expression of PDGF-D and its
XX CC proteolytic cleavage for generating an activated truncated form is useful
XX CC for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist
XX CC is useful for inhibiting tissue remodelling during the invasion of
XX CC tumour cells into normal cells. PDGF-D may be used to treat wounds,
XX CC atherosclerosis, metastasis and migration of smooth muscle cells.
XX SQ Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 other;
XX Query Match 2.0%; Score 601; DB 21; Length 2253;
XX Best Local Similarity 99.8%; Pred. No. 5.1e-173;
XX Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 GTATGCTAGAAAGCCTCATCTTTGATTTTAAATATACAAAGATGCTTTCTTTAAGAGA 60
XX DB 1812 GTATGCTAGAAAGCCTCATCTTTGATTTTAAATATACAAAGATGCTTTCTTTAAGAGA 1753
XX QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATTTATTCCTCCATAATTTT 120
XX DB 1752 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATTTATTCCTCCATAATTTT 1693
XX QY 121 CTAAGACATGTTTTCATATATTTGACCATCCCTTATTTTGGCAAGATTTTAAAGAGTCT 180
XX DB 1692 CTAAGACATGTTTTCATATATTTGACCATCCCTTATTTTGGCAAGATTTTAAAGAGTCT 1633
XX QY 181 AACTCAACATATGTAAGCTCTGCTGTAACCTGCTTATATATACCAAAAAAACAATTGAT 240
XX DB 1632 AACTCAACATATGTAAGCTCTGCTGTAACCTGCTTATATATACCAAAAAAACAATTGAT 1573
XX QY 241 CTAATACACATAGACATGAATATATTTCTGTGTGTGTTGTCATATATATAAAGCTCAAC 300
XX DB 1572 CTAATACACATAGACATGAATATATTTCTGTGTGTGTTGTCATATATATAAAGCTCAAC 1513
XX QY 301 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAACTTGTATATACCTTTCTAC 360
XX DB 1512 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAACTTGTATATACCTTTCTAC 1453
XX QY 361 TTGCCATGCGATTAAACAAAGAGGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATG 420
XX DB 1452 TTGCCATGCGATTAAACAAAGAGGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATG 1393
XX QY 421 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGCTCTTATCTCACCCTCCCTTAA 480
XX DB 1392 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGCTCTTATCTCACCCTCCCTTAA 1333
XX QY 481 ACTAAAGGTTCTTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGCTT 540
XX DB 1332 ACTAAAGGTTCTTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGCTT 1273
XX QY 541 GAGCTGCAGATACAAATCAGATCTGCTGATGATCCAACTGGATGTCACCTAGAGCCATG 600
XX DB 1272 GAGCTGCAGATACAAATCAGATCTGCTGATGATCCAACTGGATGTCACCTAGAGCCATG 1213
XX QY 601 GTCTTAGCTCTACCCCTCTCTTGTGATGTCGCCAGGCTCAAACTGTAATACCT 652
XX DB 1212 GTCTTAGCTCTACCCCTCTCTTGTGATGTCGCCAGGCTCAAACTGTAATACCT 1161
XX RESULT 8
XX AAH46939/c
XX ID AAH46939 standard; cDNA; 3798 BP.
XX AC AAH46939;
XX XX
XX DT 25-SEP-2001 (first entry)
XX DE Human secreted protein encoding. cDNA (clone Id HGCNC48).
XX KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
XX KW antiproliferative; cytosolic; cardiant; vasotropic; cerebroprotective;
XX KW neotropic; neuroprotective; antibacterial; virucide; fungicide; human;
XX KW ophthalmological; gene therapy; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200155430-A1.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01431.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 12-SEP-2000; 2000US-0231968.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
XX PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;
XX PI Ni J, Ruben SM, Barash SC;
XX DB WPI: 2001-476220/51.
```


[illegible]

Db 2422 CAGGCTAGTAGAAGTTGGTTGCTGTAGGAAAGGCTCTCTATCTCACCTCCTTAA 2481
QY 481 ACTAAGAGTCTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGCTTT 540
Db 2482 ACTATAGTCTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGCTTT 2541
QY 541 GAGCTGCAGATACAATACATCGTTTCATCGTGTGATGCCAAGTGTCAACTAGAGCCATG 600
Db 2542 GAGCTGCAGATACAATACATCGTTTCATCGTGTGATGCCAAGTGTCAACTAGAGCCATG 2601
QY 601 GTCCTAGCTCTACCCCTCTCTGTGATGGCCAGGCTCAAACTGTAATACCT 652
Db 2602 GTCCTAGCTCTACCCCTCTCTGTGATGGCCAGGCTCAAACTGTAATACCT 2653

RESULT 11

ABL63632
ID ABL63632 standard; DNA; 485 BP.

XX ABL63632;

XX 15-MAY-2002 (first entry)

XX Breast cancer related gene sequence SEQ ID NO:1969.

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.

XX 18-SEP-2000; 2000US-209531P.

XX 18-SEP-2000; 2000US-233131P.

XX 20-SEP-2000; 2000US-233617P.

XX 20-SEP-2000; 2000US-234009P.

XX 20-SEP-2000; 2000US-234034P.

XX 20-SEP-2000; 2000US-234052P.

XX 22-SEP-2000; 2000US-234509P.

XX 22-SEP-2000; 2000US-234567P.

XX 25-SEP-2000; 2000US-234923P.

XX 25-SEP-2000; 2000US-234924P.

XX 25-SEP-2000; 2000US-235077P.

XX 25-SEP-2000; 2000US-235082P.

XX 25-SEP-2000; 2000US-235134P.

XX 25-SEP-2000; 2000US-235280P.

XX 26-SEP-2000; 2000US-235637P.

XX 26-SEP-2000; 2000US-235638P.

XX 27-SEP-2000; 2000US-235711P.

XX 27-SEP-2000; 2000US-235720P.

XX 27-SEP-2000; 2000US-235840P.

PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
PI WPI; 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX Claim 1; SEQ ID 1969; 44pp; English.
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX Sequence 485 BP; 161 A; 72 C; 75 G; 177 T; 0 other;
Query Match 1.5%; Score 460; DB 24; Length 485;
Best Local Similarity 100.0%; Pred. No. 4e-130;
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 60
Db 26 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 85
QY 61 GCAAGATTCAAATTTGTTTGTGTTTCAAAATTTAAATAATTTATCTCTAAATTTT 120
Db 86 GCAAGATTCAAATTTGTTTGTGTTTCAAAATTTAAATAATTTATCTCTAAATTTT 145
QY 121 CTAAGACATGTTTCATATATTTTGACCATCCCTTATTTGGCAAGAGATTTAAGAGTCT 180
Db 146 CTAAGACATGTTTCATATATTTTGACCATCCCTTATTTGGCAAGAGATTTAAGAGTCT 205
QY 181 AACTCAACATATGTAAGCTCTGCTGCTGTTATATATACCAAAAAACATTTGAT 240
Db 206 AACTCAACATATGTAAGCTCTGCTGCTGTTATATATACCAAAAAACATTTGAT 265
QY 241 CTATATACATAGACATGAATATATTTCTGCTGTTGTTGTCATATATAACCTCAAAAC 300
Db 266 CTATATACATAGACATGAATATATTTCTGCTGTTGTTGTCATATATAACCTCAAAAC 325
QY 301 ACTATTATTAATGCAATCCCTATATCTTTAGGTATAGAGTTGATGATATACCTTTCTAC 360
Db 326 ACTATTATTAATGCAATCCCTATATCTTTAGGTATAGAGTTGATGATATACCTTTCTAC 385
QY 361 TTGCCATGCCATTACAAGCAAGCTGAGACTCAGCACTGCTGCTGTTGTTGTTGTTGTTG 420
Db 386 TTGCCATGCCATTACAAGCAAGCTGAGACTCAGCACTGCTGCTGTTGTTGTTGTTGTTG 445

QY 421 CAGGCTAGTAGTAAGTTTGGTTCGCTGGTAGGAAAGGGTC 460
|||||
Db 446 CAGGCTAGTAGTAAGTTTGGTTCGCTGGTAGGAAAGGGTC 485

RESULT 12
AAC81555/c
ID AAC81555 standard; cDNA; 1882 BP.
XX AAC81555;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human growth factor homologue zvegf4 cDNA, SEQ ID NO:1.

XX Human; zvegf4; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KW immunomodulation; hepatic; chromosome 11q22.3-23.1; ss.

XX Homo sapiens.
OS
XX WO200066736-A1.
PN
XX 09-NOV-2000.
PD
XX 03-MAY-2000; 2000WO-US40047.
PF
XX 03-MAY-1999; 99US-0304216.
PR
XX 10-NOV-1999; 99US-0164463.
PR
XX 04-FEB-2000; 2000US-0180169.
XX

PA (ZYMO) ZYMOGENETICS INC.

XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX WPI: 2000-687541/67.
DR
XX P-PSDB; AAB48653.
DR

PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischaemia, multiple sclerosis and
PT Alzheimer's disease

XX Claim 35; Page 106-110; 143pp; English.

XX The invention relates to the human growth factor homologue zvegf4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
CC fusions; expression constructs and host cells comprising human zvegf4
CC nucleic acids; the recombinant expression of human zvegf4; an antibody
CC which binds to human zvegf4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegf4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells

PR 06-JUL-1999; 99US-0142576.
PR 21-OCT-1999; 99US-0161653.
PR 12-NOV-1999; 99US-0165255.
PA (ZYMO) ZYMOGENETICS INC.
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
XX WPI; 2000-423420/36.
DR P-PSDB; AAY96864.
XX Novel zvegfg3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence
XX
PS Disclosure; Page 161-164; 173pp; English.
XX
CC Polypeptides comprising an epitope-bearing portion human or murine
CC ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The
CC growth factors comprise a growth factor domain and a CUB domain (generic
CC sequence motifs are shown in AAY96859 and AAY96860). The growth factor
CC domain is characterized by an arrangement of cysteine residues and
CC beta-strands that is characteristic of the "cysteine knot" structure of
CC the platelet-derived growth factor (PDGF) family. The CUB domain shows
CC homology to CUB domains in neurofilins, human bone morphogenetic
CC protein-1, porcine seminal plasma protein, bovine acidic seminal fluid
CC protein and Xenopus laevis tolloid-like protein. Structural analysis and
CC homology predict that ZVEGF3 polypeptides complex with a second
CC polypeptide to form multimeric proteins. The human zvegfg3 gene has been
CC mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth
CC of fibroblasts or smooth muscles cells, for activating cell surface
CC PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated
CC cellular processes. ZVEGF3 is useful for regulating (post-development)
CC organ growth, regeneration and maintenance, as well as tissue
CC maintenance and repair processes. ZVEGF3 antagonists are useful for
CC treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic
CC limb disease, peripheral vascular disease, myocardial ischemia, vascular
CC intimal hyperplasia, atherosclerosis, wound healing, chronic liver
CC disease and haemangioma formation. ZVEGF3 can also be used to modulate
CC neurite growth and development of the nervous system, and for treating
CC neurodegenerative diseases.
XX
SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

Query Match
Best Local Similarity 1.3%; Score 377; DB 21; Length 1882;
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 225 AAAAAAACATTGATCTATATACACATGACATGAATATATTTCTGTGTGTGTGTGTC 284
DB 1638 AAAAAAACATTGATCTATATACACATGACATGAATATATTTCTGTGTGTGTGTC 1579
QY 285 ATATATAACCTCAACACTATTATTAATGCAATCTATATCTTAGGTATAGAGTTGA 344
DB 1578 ATATATAACCTCAACACTATTATTAATGCAATCTATATCTTAGGTATAGAGTTGA 1519
QY 345 TGATATACCTTTCTTCTGATGCGCATTTACAAAGCAAGCTGAGACTCAGCAACCACT 404
DB 1518 TGATATACCTTTCTTCTGATGCGCATTTACAAAGCAAGCTGAGACTCAGCAACCACT 1459
QY 405 TGTGTTTCATTGCGAGGCTAGTAGTAAGTTTGTGTTGCTGGTAGGAAAGGCTCTCTT 464
DB 1458 TGTGTTTCATTGCGAGGCTAGTAGTAAGTTTGTGTTGCTGGTAGGAAAGGCTCTCTT 1399
QY 465 ATCTACCCCTCCTTAACCTAAAGGTTCTTTCAGGCTTAATTAAGGATGTCACATCTC 524
DB 1398 ATCTACCCCTCCTTAACCTAAAGGTTCTTTCAGGCTTAATTAAGGATGTCACATCTC 1339
QY 525 TTATCGAGGTGGTCTTGAGCTGCAGATACATCATCTGTTTCATGGTGATCCAACTGGAT 584
DB 1338 TTATCGAGGTGGTCTTGAGCTGCAGATACATCATCTGTTTCATGGTGATCCAACTGGAT 1279

QY 585 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGGCCAGGCTCAAACTG 644
DB 1278 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGGCCAGGCTCAAACTG 1219
QY 645 TAATACCT 652
DB 1218 TAATACCT 1211
RESULT 14
AAH47772/C
ID AAH47772 standard; cDNA; 1882 BP.
XX
AC AAH47772;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human zvegfg4 polypeptide encoding cDNA.
XX
KW zvegfg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;
KW bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis;
KW osteopathic; vulnery; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 226..1338
FT /*tag= a
FT /*product= "zvegfg4 protein"
FT sig_peptide 226..279
FT /*tag= b
FT mat_peptide 280..1335
FT /*note= "secretory peptide"
FT /*tag= c
XX
PW WO200157083-A1.
XX
XX 09-AUG-2001.
XX
XX 03-MAY-2000; 2000WO-US12095.
XX
XX 04-FEB-2000; 2000US-180169P.
XX 31-MAR-2000; 2000US-0540224.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbertson DG, Hart CE;
XX
XX WPI; 2001-611088/70.
XX P-PSDB; AAG65601.
XX
XX Use of zvegfg4 polypeptide for promoting bone, ligament or cartilage
XX growth in mammal at site of fracture, implant, and bone graft, and for
XX promoting growth or differentiation of osteoblasts, chondrocytes in
XX culture
XX
XX Example 1; Page 44-47; 57pp; English.
XX
XX The invention relates to the use of zvegfg4 polypeptide for promoting
XX bone, ligament or cartilage growth in a mammal, and for promoting
XX proliferation or differentiation of osteoblasts, osteoclasts,
XX chondrocytes or bone marrow stem cells in culture. For promoting
XX cartilage growth, chondrocytes are cultured ex vivo in presence of the
XX zvegfg4 polypeptide and then placed into mammal where cartilage is to be
XX grown. Zvegfg4 polypeptide is useful for promoting growth of bone,
XX ligament or cartilage in a mammal at a site of bony defect such as
XX fracture, bone graft, implant or periodontal pocket, in humans and non-
XX human animals such as domestic animals including livestock and companion
XX animals. Zvegfg4 is used for promoting growth of bone, ligament, or
XX cartilage in conditions of bone defects following therapeutic treatments
XX of bone cancers or other conditions characterized by increased bone loss
XX or decreased bone formation, or elevation of peak bone mass in pre-
XX menopausal woman. It is also useful for healing bone following radiation

CC -induced osteonecrosis, repairing bone defects arising from surgery, and
CC promotion of bone healing in plastic surgery, increasing bone formation
CC during distraction osteogenesis, treating bone injuries including repair
CC of cartilage and ligament and treatment of osteoporosis. The present
CC sequence represents a human zvegfg4 polypeptide encoding cDNA.

xx
SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

Query Match 1.3%; Score 377; DB 22; Length 1882;
Best Local Similarity 99.8%; Pred. No. 4.4e-105;
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 225 AAAAAAACATTTGATCTATATACACATAGACATGAATATTTCTGTGTGTTTGTGC 284
Db AAAAAAACATTTGATCTATATACACATAGACATGAATATTTCTGTGTGTTTGTGC 1579

Qy 285 ATATATAACCTCAACACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGA 344
Db ATATATAACCTCAACACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGA 1519

Qy 345 TGATATACCTTTCTACTTGCATGGCATTAAACAAGCAAGGCTGAGACTCAGCAACCACT 404
Db TGATATACCTTTCTACTTGCATGGCATTAAACAAGCAAGGCTGAGACTCAGCAACCACT 1459

Qy 405 TGTGTTTCATTCAGCTCAGGCTAGTAGTAAGTTGGTTGGTGGTGGTGGTGGTGGTGGT 464
Db TGTGTTTCATTCAGCTCAGGCTAGTAGTAAGTTGGTTGGTGGTGGTGGTGGTGGTGGT 1399

Qy 465 ATCTCACCCCTTAACTAAAGTCTTTTCAGGCTTAATGTAAGGATGCGCATTTCTC 524
Db ATCTCACCCCTTAACTAAAGTCTTTTCAGGCTTAATGTAAGGATGCGCATTTCTC 1339

Qy 525 TTATCGAGGTGGTCTTTCAGCTGCGATACATCATCTGTTGATGGTGATCCAACTGGAT 584
Db TTATCGAGGTGGTCTTTCAGCTGCGATACATCATCTGTTGATGGTGATCCAACTGGAT 1279

Qy 585 GTCAACTAGAGCCCATGCTTTAGCTCTACCCCTCTCTTGTATGGCCAGGCTCAAACTG 644
Db GTCAACTAGAGCCCATGCTTTAGCTCTACCCCTCTCTTGTATGGCCAGGCTCAAACTG 1219

Qy 645 TAATACTT 652
Db TAATACTT 1211

RESULT 15
ABQ73239/c

ID ABQ73239 standard; cDNA; 1882 BP.
xx
AC ABQ73239;
xx

DT 30-SEP-2002 (first entry)
xx
DE Human zvegfg4 encoding cDNA SEQ ID NO:1.

xx Human; zvegfg4; cell proliferation; extracellular matrix production;
xx fibroproliferative disorder; PDGF-D; platelet derived growth factor;
xx PDGF; vascular endothelial growth factor; VEGF; cytoskeletal; nephrotropic;
xx hepatotropic; antiinflammatory; osteopathic; antiarthritic; metastasis;
xx prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis;
xx diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome;
xx chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis;
xx hyperostosis; osteoarthritis; gene; ss.

xx Homo sapiens.
xx

xx Key Location/Qualifiers
xx CDS 226..1338
xx /*tag= a
xx /product= "zvegfg4"

xx US2002064832-A1
xx

PD 30-MAY-2002.

xx 14-MAR-2001; 2001US-0808972.

xx 03-MAY-1999; 99US-132250P.

xx 10-NOV-1999; 99US-164463P.

xx 04-FEB-2000; 2000US-180169P.

xx 26-SEP-2000; 2000US-235295P.

xx 03-MAY-2000; 2000US-0564595.

xx (HART/) HART C E.

xx (TOPO/) TOPOUZIS S.

xx (GILB/) GILBERTSON D G.

xx Hart CE, Topouzis S, Gilbertson DG;

xx WPI; 2002-573696/61.

xx P-PSDB; ABP51640.

xx Reducing proliferation or extracellular matrix production by a cell in
xx a mammal, useful for treating fibroproliferative disorders of bone,
xx liver and kidney, comprises administering a zvegfg4 antagonist -

xx Example 1; Page 18-19; 34pp; English.

xx The present invention describes a method for reducing proliferation of
xx extracellular matrix production by a cell in a mammal. The method
xx comprises administering to the mammal a composition comprising a
xx therapeutically effective amount of a zvegfg4 antagonist chosen from
xx anti-zvegfg4 antibodies, inhibitory polynucleotides, inhibitors of
xx zvegfg4 activation, and mitogenically inactive, receptor-binding variants
xx of zvegfg4. zvegfg4 (also called PDGF-D) is a multi-domain protein that is
xx structurally related to platelet derived growth factor (PDGF) and
xx vascular endothelial growth factors (VEGF). zvegfg4 has cytoskeletal,
xx nephrotropic, hepatotropic, antiinflammatory, osteopathic and
xx antiarthritic activities. The method is useful for reducing proliferation
xx of mesangial, epithelial, endothelial, smooth muscle, fibroblast,
xx osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells
xx in a mammal, in particular proliferation of prostate tumour cells, and
xx for reducing extracellular matrix production by a cell in a mammal
xx suffering from a fibroproliferative disorder of kidney, bone or liver.

xx In particular it is useful for reducing stellate cell activation. The
xx method is useful for reducing metastasis of prostate cancer cells to
xx bone in a mammal and for treating a fibroproliferative disorder of
xx kidney, liver or bone in a mammal. Fibroproliferative disorders of the
xx kidney include, glomerulonephritis, diabetic glomerulosclerosis, lupus
xx nephritis, renal arteriosclerosis and nephrotic syndrome, disorders of
xx the liver include chronic active hepatitis and many other types of
xx cirrhosis, and disorders of the bone include osteopetrosis, hyperostosis,
xx osteosclerosis, osteoarthritis, and ectopic bone formation in metastatic
xx prostate cancer. The present sequence encodes human zvegfg4, which is
xx used in an example from the present invention.

xx Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

xx Query Match 1.3%; Score 377; DB 24; Length 1882;
xx Best Local Similarity 99.8%; Pred. No. 4.4e-105;
xx Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 225 AAAAAAACATTTGATCTATATACACATAGACATGAATATTTCTGTGTGTTTGTGC 284
Db AAAAAAACATTTGATCTATATACACATAGACATGAATATTTCTGTGTGTTTGTGC 1579

Qy 285 ATATATAACCTCAACACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGA 344
Db ATATATAACCTCAACACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGA 1519

Qy 345 TGATATACCTTTCTACTTGCATGGCATTAAACAAGCAAGGCTGAGACTCAGCAACCACT 404
Db TGATATACCTTTCTACTTGCATGGCATTAAACAAGCAAGGCTGAGACTCAGCAACCACT 1459

Qy 405 TGTGTTTCATTCAGGCTAGTAGTAAGTTGGTTGGTGGTGGTGGTGGTGGTGGT 464
Db TGTGTTTCATTCAGGCTAGTAGTAAGTTGGTTGGTGGTGGTGGTGGTGGTGGT 1579

Db 1458 TGTGTTTCATTGATCCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAAGGGTCTCTT 1399
QY 465 ATCTCACCCCTCCTTAAACTAAAGGTTCTTTTCAGGCTTAAATGTAAGGATGTGCACATTCTC 524
Db 1398 ATCTCACCCCTCCTTAAACTAAAGGTTCTTTTCAGGCTTAAATGTAAGGATGTGCACATTCTC 1339
QY 525 TTATCGAGGTGGTCTTGGAGCTGCAGATACAAATCACATCCTTCATGGTGATCCAACTGGAT 584
Db 1338 TTATCGAGGTGGTCTTGGAGCTGCAGATACAAATCGCATCGTTTCATGGTGATCCAACTGGAT 1279
QY 585 GTCAACTAGAGCATGGTCTTAGCTCTACCCCTCCTCTTGTGATGTGCCAGGCTCAAACCTG 644
Db 1278 GTCAACTAGAGCATGGTCTTAGCTCTACCCCTCCTCTTGTGATGTGCCAGGCTCAAACCTG 1219
QY 645 TAATACCT 652
Db 1218 TAATACCT 1211

Search completed: July 7, 2003, 07:56:26
Job time : 3758 secs

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 05:44:16 ; Search time 23547 Seconds

(without alignments)

20579.486 Million cell updates/sec

Title: US-10-083-853B-2

Perfect score: 29921

Sequence: 1 gatatgtgaagaagctca.....caatttgtgaagaagtaa 29921

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:**
 - 2: em_esthum:**
 - 3: em_estin:**
 - 4: em_estnu:**
 - 5: em_estov:**
 - 6: em_estpl:**
 - 7: em_estro:**
 - 8: em_htc:**
 - 9: gb_est1:**
 - 10: gb_est2:**
 - 11: gb_htc:**
 - 12: gb_est3:**
 - 13: gb_est4:**
 - 14: gb_est5:**
 - 15: em_estfun:**
 - 16: em_estom:**
 - 17: gb_gss:**
 - 18: em_gss_hum:**
 - 19: em_gss_inv:**
 - 20: em_gss_pln:**
 - 21: em_gss_vrt:**
 - 22: em_gss_fun:**
 - 23: em_gss_mam:**
 - 24: em_gss_mus:**
 - 25: em_gss_other:**
 - 26: em_gss_pro:**
 - 27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	652	2.2	3739	11 AF113216	AF113216 Homo sapi
C 2	572	1.9	606	14 BQ575044	BQ575044 UI-H-EZ1-
C 3	460	1.5	485	9 AA488996	AA488996 aa54cl0.s
C 4	431	1.4	482	9 AI799086	AI799086 we98b03.x
C 5	367	1.2	582	10 AW977062	AW977062 EST389171
C 6	337	1.1	407	9 AA748556	AA748556 aa57b11.s

7	263	0.9	505	10	AW274723	AW274723
C 8	244	0.8	560	17	AW968905	AW968905 EST380981
C 9	241	0.8	926	17	BQ3230	BQ3230 CSRL-173C3-
C 10	197	0.7	248	9	AA491122	AA491122 aa46g03.r
C 11	187	0.6	452	17	AQ633340	AQ633340 RPCI-11-4
C 12	185	0.6	360	9	AA488780	AA488780 aa54cl0.f
C 13	163	0.5	406	9	AI221902	AI221902 q999h07.x
C 14	158	0.5	187	9	AA721242	AA721242 nz72c08.s
C 15	155	0.5	363	17	AQ111794	AQ111794 CIT-HSP-2
C 16	155	0.5	425	10	AW467833	AW467833 bs26e05.x
C 17	155	0.5	651	17	AQ425649	AQ425649 CITBI-E1-
C 18	155	0.5	684	17	AG106397	AG106397 Pan trogl
C 19	155	0.5	710	9	AI401148	AI401148 tg26e01.x
C 20	154	0.5	321	9	AA501789	AA501789 ng19a10.s
C 21	154	0.5	321	9	AA501810	AA501810 ng19c10.s
C 22	153	0.5	217	9	AI570720	AI570720 tr66a05.x
C 23	151	0.5	415	17	B43028	B43028 HS-1057-A1-
C 24	149	0.5	393	12	BF873398	BF873398 QV2-ET010
C 25	149	0.5	401	17	AQ588612	AQ588612 CITBI-E1-
C 26	149	0.5	420	17	AQ016093	AQ016093 CIT-HSP-2
C 27	149	0.5	447	9	AI628588	AI628588 ty76g10.x
C 28	149	0.5	522	17	AQ113830	AQ113830 CIT-HSP-2
C 29	149	0.5	658	12	BG572024	BG572024 602592482
C 30	149	0.5	690	17	AG081126	AG081126 Pan trogl
C 31	149	0.5	692	10	AV730945	AV730945 AV730945
C 32	149	0.5	703	17	AG040534	AG040534 Pan trogl
C 33	149	0.5	1052	11	BC032807	BC032807 Homo sapi
C 34	148	0.5	411	10	AW864612	AW864612 PK3-SN001
C 35	147	0.5	735	9	AL704192	AL704192 DKFZP886H
C 36	146	0.5	467	13	BMI44799	BMI44799 TCAAPID13
C 37	144	0.5	640	9	AL157589	AL157589 DKFZP761H
C 38	143	0.5	434	12	BF446725	BF446725 7q91c04.x
C 39	143	0.5	464	9	AI630984	AI630984 tx54b12.x
C 40	143	0.5	517	10	BE670185	BE670185 7e31c08.x
C 41	141	0.5	668	17	AG122980	AG122980 Pan trogl
C 42	139	0.5	506	17	AQ401567	AQ401567 HS-5067_A
C 43	138	0.5	645	12	BF916874	BF916874 IL3-UT011
C 44	136	0.5	594	17	AQ392781	AQ392781 CITBI-E1-
C 45	135	0.5	561	17	AQ826679	AQ826679 HS_5300_A

ALIGNMENTS

RESULT 1	AF113216/c	AF113216	3739 bp	mrna	linear	HTC 12-APR-2002
LOCUS	AF113216	Homo sapiens	MSTP036	mrna	complete cds	
DEFINITION	AF113216	Homo sapiens	MSTP036	mrna	complete cds	
ACCESSION	AF113216	Homo sapiens	MSTP036	mrna	complete cds	
VERSION	AF113216.1	GI:11640579				
KEYWORDS	HTC					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 3739)					
AUTHORS	Liu, B., Liu, Y.O., Wang, X.Y., Zhao, B., Sheng, H., Zhao, X.W., Liu, S., Cao, H.Q., Zhao, Y., Liu, L.S., Zhang, C.L., Zhang, J., Wei, Y.J., Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.					
TITLE	Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R. China					
JOURNAL	Location/Qualifiers					
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Db      395 TTGCCATGGCATTAAACAAAGAGCTGAGACTCAGCAACCACTTCTGTTCATTGCGATTG 454
QY      421 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGGTCTCTATCTCTCACCCCTCTTAA 480
Db      455 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGGTCTCTATCTCTCACCCCTCTTAA 514
QY      481 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATTCCTCTATCGAGGTGCTTT 540
Db      515 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATTCCTCTATCGAGGTGCTTT 574
QY      541 GAGCTGCAGATACAATCACATCCTTCATGGTG 572
Db      575 GAGCTGCAGATACAATCACATCCTTCATGGTG 606

RESULT 3
LOCUS   AA488996
DEFINITION aa54c10.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:824754 3',
          mRNA sequence.
ACCESSION AA488996
VERSION   AA488996.1 GI:2218598
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT   Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaps-r@mail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
          Ph.D., Gerald Marti, M.D.
          CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
          CDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www.bio.llnl.gov/bbrp/image/image.html
          Seq primer: -41ml3 fwd. Er from Amersham
          High quality sequence stop: 465.
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                 /tissue_type="germinal center B cell"
                 /lab_host="DH10B"
                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                 was prepared from human tonsillar cells enriched for
                 germinal center B cells by flow sorting (CD20+, IgD-),
                 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                 primed with a Not I - oligo(dT) primer
                 [5'-GTTTACCATCTGAAGTGGGAGCGCGCTCATTTTCTTTT-3'
                 ]. Double-stranded cDNA was ligated to Eco RI adaptors
                 (Pharmacia), digested with Not I and cloned into the Not I
                 and Eco RI sites of the modified pT7T3 vector. Library
                 went through one round of normalization, and was
                 constructed by Bento Soares and M. Fatima Bonaldo."
         161 a 72 c 75 g 177 t

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Query Match      1.5%; Score 460; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATATGTAGAAAGCCTCATCTTTTTCATTTTAAATATACAAAGATGCTTTCTTTAAGAGA 60
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QY      61 GCAAGATTCAAAATTTCTTTTGTCTTCAAAATTTAAATAATATATCTCTCTAAATTTT 120
Db      86 GCAAGATTCAAAATTTCTTTTGTCTTCAAAATTTAAATAATATATCTCTCTAAATTTT 145
QY      121 CTAAGACATGTTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT 180
Db      146 CTAAGACATGTTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT 205
QY      181 AACTCAACATATGTAAGCTCTGGTGTACCTGGTTATATATATACCAAAAAAACAATTGTAT 240
Db      206 AACTCAACATATGTAAGCTCTGGTGTACCTGGTTATATATATACCAAAAAAACAATTGTAT 265
QY      241 CTATATACACATAGACATGAATATATTTCTGTCTGTGTTTGTGCATATATATAAACCCTCAAAC 300
Db      266 CTATATACACATAGACATGAATATATTTCTGTCTGTGTTTGTGCATATATATAAACCCTCAAAC 325
QY      301 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 360
Db      326 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 385
QY      361 TTGCCATGGCATTAAACAAAGAGCTGAGACTCAGCAACCACTTGTGTTTCATTGCGATTG 420
Db      386 TTGCCATGGCATTAAACAAAGAGCTGAGACTCAGCAACCACTTGTGTTTCATTGCGATTG 445
QY      421 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGGTC 460
Db      446 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGGTC 485

RESULT 4
LOCUS   AI799066/c
DEFINITION we98b03.x1 Soares_NFL_T_GCB.S1 Homo sapiens cDNA clone
          IMAGE:2349101 3' similar to contains OFR.T1 OFR repetitive element
          ;, mRNA sequence.
ACCESSION AI799066
VERSION   AI799066.1 GI:5364538
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT   Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaps-r@mail.nih.gov
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert Length: 825 Std Error: 0.00
          Seq primer: -400P from Gibco
          High quality sequence stop: 476.
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                 /lab_host="DH10B"
                 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
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                 Equal amounts of plasmid DNA from three normalized
                 libraries (fetal lung NBHL19W, testis NHT, and B-cell

```

NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 121 a 122 c 89 g 149 t 1 others
ORIGIN

Query Match 1.4%; Score 431; DB 9; Length 482;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25345 AAGACTGGTACTTATTAAGAAAGAGGTTTAATGCGCTCACAGTTATGCTATGCGCTGG 25404
Db |||||||
482 AAGACTGGGTAGTTTATAAAGAAAGAGGTTTAATGCGCTCACAGTTATGCTATGCGCTGG 423
QY 25405 GAGGCTTAAGAAACTTACAATCATGCCAGAGGCGAAGGAGCAAGGACACGCTCTTA 25464
Db |||||||
422 GAGGCTTAAGAAACTTACAATCATGCCAGAGGCGAAGGAGCAAGGACACGCTCTTA 363
QY 25465 CATGTGGCAGGAGGAGAGCATGTGTGCAAGTGTAGGGGAACTGCCCTTTATAAAATCA 25524
Db |||||||
362 CATGTGGCAGGAGGAGAGCATGTGTGCAAGTGTAGGGGAACTGCCCTTTATAAAATCA 303
QY 25525 TCAGATCTTGTGCCACTCACTCACTATCACAGATAGCATGGGAAACCACTCCCATG 25584
Db |||||||
302 TCAGATCTTGTGCCACTCACTCACTATCACAGATAGCATGGGAAACCACTCCCATG 243
QY 25585 ATTCAATTATCTCCATCTTGTTCCTCCCTTGACATGTGGGGATTATGGGGATTATGGGA 25644
Db |||||||
242 ATTCAATTATCTCCATCTTGTTCCTCCCTTGACATGTGGGGATTATGGGGATTATGGGA 183
QY 25645 TTGCAATTCAAGATGAGATTGGGTGGGACACATGCAATGCAATCTATTAGCAAGTAAG 25704
Db |||||||
182 TTGCAATTCAAGATGAGATTGGGTGGGACACATGCAATGCAATCTATTAGCAAGTAAG 123
QY 25705 ACACCTCAGTGAGTGTGATCTCTCAGCAGCAGGCGCTTACAGCATATATCTCTAGGA 25764
Db |||||||
122 ACACCTCAGTGAGTGTGATCTCTCAGCAGCAGGCGCTTACAGCATATATCTCTAGGA 63
QY 25765 GCAGTGTAGTGTCTCTTAAGTCTAGTGGGGCATAAAGGAAACCAATCCCATTAATTT 25824
Db |||||||
62 GCAGTGTAGTGTCTCTTAAGTCTAGTGGGGCATAAAGGAAACCAATCCCATTAATTT 3
QY 25825 TC 25826
Db ||
2 TC 1

RESULT 5
AW977062
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW977062 582 bp mRNA linear EST 02-JUN-2000
EST389171 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
AW977062
AW977062.1 GI:8168303
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Heide, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeaman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@igr.org
Plate: 371
Seq primer: Forward.

FEATURES
Source
Location/Qualifiers
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/clone_lib="MAGE resequences, MAGO"
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Matches 417; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 TATTTTGTCTATCTTTATTTGTCGCAAAATTTATTTAAATGATATATTAAGTTTTCG 60
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241 TCAGATAGGATTAACCTGTCATCAGGACACTTGGCTTGGGCAAACTAGTGTGGTAGAA 300
QY 17606 TTTCTGCTCCTTAATCAAAACCTCGCTGGTGGTGGCTTGTGCACTGAACCACTGAACAAC 17665
Db |||||||
301 TTTCTGCTCCTTAATCAAAACCTCGCTGGTGGTGGCTTGTGCACTGAACCACTGAACAAC 360
QY 17666 GTATCAATGCGCTCTCTTCTGTAATCTTATAGATTAAAGCATTCACAAGAAATCT 17723
Db |||||||
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RESULT 6
AA748556
LOCUS
DEFINITION

AA748556 407 bp mRNA linear EST 27-JAN-1998
oa57b11.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309053 3',
mRNA sequence.
AA748556
AA748556.1 GI:2788514
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html
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High quality sequence stop: 389.

FEATURES
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polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(GT) primer
(5'-TGTTACCAATCGAAGTGGAGCGCGCTCATTTTCTTTT-3',
I). Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
108 a 72 c 71 g 156 t

BASE COUNT
ORIGIN

Query Match 1.1%; Score 337; DB 9; Length 407;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 17362 TTGCTTATGAGATTGTGCCGTATATCTCTGAATGAATTAACATCATATATTCCTCTTTT 17421
Db 74 TTGCTTATGAGATTGTGCCGTATATCTCTGAATGAATTAACATCATATATTCCTCTTTT 133
QY 17422 TCTGCTTTCTGCAAGTAGTCAAGCTCTGAATTTACTGTATACATATTTGATATATA 17481
Db 134 TCTGCTTTCTGCAAGTAGTCAAGCTCTGAATTTACTGTATACATATTTGATATATA 193
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QY 17542 TTGCTCAGATAGATTAACTGTCTATCAGGACACTTGGCTTGGCAAACTAGTGTGGGT 17601
Db 254 TTGCTCAGATAGATTAACTGTCTATCAGGACACTTGGCTTGGCAAACTAGTGTGGGT 313
QY 17602 AGAATTTCTGCTCCTTAATCAAACTGGGCTGGGCTTGTGCAGTGAACACCTGAAC 17661
Db 314 AGAATTTCTGCTCCTTAATCAAACTGGGCTGGGCTTGTGCAGTGAACACCTGAAC 373
QY 17662 AACTGTATGCAATGGCCCTCTCTCTG 17689
Db 374 AACTGTATGCAATGGCCCTCTCTCTG 401

RESULT 7
LOCUS

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DEFINITION xn34502.x1 NCI_CGAP_kid11 Homo sapiens cDNA clone IMAGE:2695563 3',
mRNA sequence.
ACCESSION AW274723
VERSION AW274723.1 GI:6661753
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 475.

FEATURES
source

Location/Qualifiers
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/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
169 a 83 c 75 g 178 t

BASE COUNT
ORIGIN

Query Match 0.9%; Score 263; DB 10; Length 505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 AAAAAAACATTTGATCTATATACATAGACATGAATATTTCTGTGTGTTGTC 284
Db 243 AAAAAAACATTTGATCTATATACATAGACATGAATATTTCTGTGTGTTGTC 302
QY 285 ATATATAACCTCAACACTATTAATGAATCCCTATATTTCTAGGTATAGAAGTTGA 344
Db 303 ATATATAACCTCAACACTATTAATGAATCCCTATATTTCTAGGTATAGAAGTTGA 362
QY 345 TGATATACCTTTCTACTTGGCCATTAACAAGCAAGCTGAGACTCAGCAACCACT 404
Db 363 TGATATACCTTTCTACTTGGCCATTAACAAGCAAGCTGAGACTCAGCAACCACT 422
QY 405 TGTGTTTCATTCGCTTTCAGGCTAGTAGTAAGTTTGGTTGCTGTAGGAAAAGGTCCTTT 464
Db 423 TGTGTTTCATTCGCTTTCAGGCTAGTAGTAAGTTTGGTTGCTGTAGGAAAAGGTCCTTT 482
QY 465 ATCTCACCCCTCTTAAACTAAAG 487
Db 483 ATCTCACCCCTCTTAAACTAAAG 505

RESULT 8
LOCUS

AW968905/c
DEFINITION EST380981 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
ACCESSION AW968905
VERSION AW968905.1 GI:8158746
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -28ml3 rev1 Et from Amersham
 High quality sequence stop: 141.
 Location/Qualifiers

FEATURES

1. 248
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="824020"
 /clone_lib="NCI-CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 15'-TGTACCAACTGAGTGGAGCGCGCTCATTTTTTTTTTTTTTT-3'
 1). Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 75 a 56 c 42 g 75 t

BASE COUNT
 ORIGIN

Query Match 0.7%; Score 197; DB 9; Length 248;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 14542 TGACACATCTCAAGGATATTCAGAGTCTCAGGGGCATATGACAGGAGTGTGTTCCCA 14601
 DB 248 TGACACATCTCAAGGATATTCAGAGTCTCAGGGGCATATGACAGGAGTGTGTTCCCA 189
 QY 14602 GGTAGCAGTACTGCGTGGTGATGATGTTATTTTCCCTTCATCCAGCAGTGCAG 14661
 DB 188 GGTAGCAGTACTGCGTGGTGATGATGTTATTTTCCCTTCATCCAGCAGTGCAG 129
 QY 14662 AGTGATTTATAGAGCTTTGACAGTCTTAGAAGTAAATATAGGACACATGCTTAA 14721
 DB 128 AGTGATTTATAGAGCTTTGACAGTCTTAGAAGTAAATATAGGACACATGCTTAA 69
 QY 14722 AGAGATGCTTTAGATACAGTTTCAAGGATGCCAATGTTTCAATPCCACTCATCGAGCT 14781
 DB 68 AGAGATGCTTTAGATACAGTTTCAAGGATGCCAATGTTTCAATPCCACTCATCGAGCT 9
 QY 14782 AACAAAGA 14789
 DB 8 AACAAAGA 1

RESULT 11
 A0633340/c
 LOCUS A0633340 452 bp DNA linear GSS 17-JUN-1999
 DEFINITION RPCI-11-475J2.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-475J2,
 DNA sequence.
 ACCESSION A0633340
 VERSION A0633340.1 GI:5095975
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 452)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 ,J.C.
 TITLE use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building

JOURNAL COMMENT

Unpublished (1997)
 Other_GSSs: RPCI-11-475J2.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1. 452
 /organism="Homo sapiens"
 /db_xref="GDB:7682233"
 /db_xref="taxon:9606"
 /clone="RPCI-11-475J2"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 159 a 76 c 82 g 132 t 3 others

BASE COUNT
 ORIGIN

Query Match 0.6%; Score 187; DB 17; Length 452;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 18435 AATGTAATAAGAAAAGGGTTTATGTTTATTTTAACTTCAAAAGTTAATCAACATGTTA 18494
 DB 404 AATGTAATAAGAAAAGGGTTTATGTTTATTTTAACTTCAAAAGTTAATCAACATGTTA 345
 QY 18495 GAGAAATGATTTTTTGTGTGAATATGTCATATTTTGACACTGGGTCCTAGATGG 18554
 DB 344 GAGAAATGATTTTTTGTGTGAATATGTCATATTTTGACACTGGGTCCTAGATGG 285
 QY 18555 CAGTATACATAGTGGTTTAACTGCTTTGGAGCCGAGTAAAGTTACAACTGCCTTCAATC 18614
 DB 284 CAGTATACATAGTGGTTTAACTGCTTTGGAGCCGAGTAAAGTTACAACTGCCTTCAATC 225
 QY 18615 ACATCATGGCTATGTTTCCCTTTTATGTTGGAAGTTATTTAATGCTCTGAACCTTCTGCTT 18674
 DB 224 ACATCATGGCTATGTTTCCCTTTTATGTTGGAAGTTATTTAATGCTCTGAACCTTCTGCTT 165
 QY 18675 CCTCATCTATACATGTAATCATTTGAAGATTTGAATTAAGTAACTGACCTG 18723
 DB 164 CCTCATCTATACATGTAATCATTTGAAGATTTGAATTAAGTAACTGACCTG 116

RESULT 12
 AA488780/c
 LOCUS AA488780 360 bp mRNA linear EST 15-AUG-1997
 DEFINITION aa54c10.r1 NCI-CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824754 5',
 mRNA sequence.
 ACCESSION AA488780
 VERSION AA488780.1 GI:2218382
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28m13 rev1 Er from Amersham
High quality sequence stop: 358.

FEATURES

source

1. .360
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:824754"
/clone_lib="NCI-CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCATCTGCAAGTGGGCGGCTCATTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

ORIGIN

108 a 77 c 86 g 89 t

Query Match

Best Local Similarity 0.6%; Score 185; DB 9; Length 360;

Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

366 ATGCATTACAAAGCAGGCTGAGACTCAGCAACCACTTGTGTTTCATTCGATGAGGC 425

Db

360 ATGCATTACAAAGCAGGCTGAGACTCAGCAACCACTTGTGTTTCATTCGATGAGGC 301

QY

426 TAGTAGTAAGTGGTGGTGGTAGGAAAGGGTCTTATCTCACCTCCTTAAACTAA 485

Db

300 TAGTAGTAAGTGGTGGTGGTAGGAAAGGGTCTTATCTCACCTCCTTAAACTAA 241

QY

486 AGGTCTTTCAGGCTTAATGTAAGGATGTCACATTCCTTATCGAGGTGGTCTTGAGCT 545

Db

240 TGGTCTTTCAGGCTTAATGTAAGGATGTCACATTCCTTATCGAGGTGGTCTTGAGCT 181

QY

546 GCAGATCAATCATCGTTTCATGGTGCATCCACTGCATGCATAGACCATGCTCTT 605

Db

180 GCAGATCAATCATCGTTTCATGGTGCATCCACTGCATGCATAGACCATGCTCTT 121

QY

606 AGCTTACCCCTCTCTTGTATGGCCAGGCTCAAACTGTAATACCT 652

Db

120 AGCTTACCCCTCTCTTGTATGGCCAGGCTCAAACTGTAATACCT 74

RESULT 13

AI221902

LOCUS

DEFINITION AI221902 406 bp mRNA linear EST 30-NOV-1998

GG99H07.x1 Soares_NFL_T-GBC_S1 Homo sapiens cDNA clone

IMAGE:1843357.3', mRNA sequence.

ACCESSION

AI221902

VERSION

AI221902.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the INRG Consortium (info@image.llnl.gov) for further information.
Insert length: 902 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 394.

FEATURES

source

1. .406
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1843357"
/clone_lib="Soares_NFL_T-GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

ORIGIN

146 a 62 c 52 g 146 t

Query Match

Best Local Similarity 0.5%; Score 163; DB 9; Length 406;

Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

225 AAAAAAACATTTGATCTATATACATACATAGACATGATATATTTCTGTGTGTGTGC 284

Db

244 AAAAAAACATTTGATCTATATACATACATAGACATGATATTTCTGTGTGTGTGC 303

QY

285 ATATATAACCTCAAAACACTATTATTAATGCAATCTCTATATTTCTAGGTATAGAAGTTGA 344

Db

304 ATATATAACCTCAAAACACTATTATTAATGCAATCTCTATATTTCTAGGTATAGAAGTTGA 363

QY

345 TGATATACCTTCTTCTTCTGCGCATTTAAACAAGCAAGGCT 387

Db

364 TGATATACCTTCTTCTTCTGCGCATTTAAACAAGCAAGGCT 406

RESULT 14

AA721242

LOCUS

DEFINITION

AA721242

ACCESSION

AA721242

VERSION

AA721242.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1250 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 65.

FEATURES

Location/Qualifiers

1..187
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1301006"
/clone_lib="NCI CGAP GCb1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+ IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCGCTCATTTTTTTTTTTT-3'
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

49 a 24 c 23 g 91 t

Query Match

0.5%; Score 158; DB 9; Length 187;

Best Local Similarity

100.0%; Pred. No. 0;

Matches 158; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

Qy 17302

TTTATATTTGCTATCTTTATTGTCACAAATTTATTAATGATATTAATTAAGGTT 17361

Db 14

TTTATATTTGCTATCTTTATTGTCACAAATTTATTAATGATATTAATTAAGGTT 73

Qy 17362

TTCCTTATGAGATGTGCGGTGATATCTCTAAATGAATAACATCATATTCTCTTTT 17421

Db 74

TTCCTTATGAGATGTGCGGTGATATCTCTAAATGAATAACATCATATTCTCTTTT 133

Qy 17422

TCGTCTTTCTGCAAGTAGTCAAGCTCTGAATTACT 17459

Db 134

TCGTCTTTCTGCAAGTAGTCAAGCTCTGAATTACT 171

RESULT 15

AQ111794/c

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

363 bp DNA linear GSS 29-AUG-1998
CIT-HSP-2379H19.TF CIT-HSP Homo sapiens genomic clone 2379H19, DNA
GI:3488451
human.
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 363)
Adams,M.D.; Rounsley,S.D.; Zhao,S.; Bass,S.; Linher,K.; Golden,K.;
Berry,K.; Granger,D.; Suh,E.; Wible,C.; Shizuya,H.; Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other_GSSs::CIT-HSP-2379H19.TR
Contact: Mark Adams
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

Location/Qualifiers

1..363
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2379H19"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

BASE COUNT

142 a 83 c 65 g 73 t

Query Match

0.5%; Score 155; DB 17; Length 363;

Best Local Similarity

100.0%; Pred. No. 0;

Matches 155; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

Qy 29325

GTTCCTGTTTCACCTCTGATGTTCTTTTCTGCTGTCAGAACCTCTTTAGTTAATTA 29384

Db 348

GTTCCTGTTTCACCTCTGATGTTCTTTTCTGCTGTCAGAACCTCTTTAGTTAATTA 289

Qy 29385

GATCCCATTTGTCAATTTTGGCTTTTGTGCCATTTGCTTTGGTGTGTTTGTAGACATGAAGT 29444

Db 288

GATCCCATTTGTCAATTTTGGCTTTTGTGCCATTTGCTTTGGTGTGTTTGTAGACATGAAGT 229

Qy 29445

CTTTGCCCATGCGCTATGCTCTGAATGTTATGCTT 29479

Db 228

CTTTGCCCATGCGCTATGCTCTGAATGTTATGCTT 194

Search completed: July 8, 2003, 03:58:37

Job time : 23556 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 05:16:49 ; Search time 48544 Seconds
(without alignments)
17938.057 Million cell updates/sec

Database: GenBank
Sequence: 1 gatatgtgaagaagcctca.....caattctggaagaagtaa 29921

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: GenBank
Sequence: 1 gatatgtgaagaagcctca.....caattctggaagaagtaa 29921

2: gb.htg:*

3: gb.in.*

4: gb.ov.*

5: gb.pat.*

6: gb.ph.*

7: gb.pl.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.ba.*

15: em.fun.*

16: em.hum.*

17: em.in.*

18: em.mu.*

19: em.om.*

20: em.ov.*

21: em.pat.*

22: em.ph.*

23: em.pl.*

24: em.ro.*

25: em.sts.*

26: em.un.*

27: em.vi.*

28: em.htg_hum.*

29: em.htg_inv.*

30: em.htg_other.*

31: em.htg_mus.*

32: em.htg_pln.*

33: em.htg_rod.*

34: em.htg_man.*

35: em.htg_vrt.*

36: em.sy.*

37: em.htgo_hum.*

38: em.htgo_mus.*

39: em.htgo_other.*

40: em.htgo_hum.*

41: em.htgo_mus.*

42: em.htgo_other.*

43: em.htgo_hum.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26958	90.1	182403	2	AC024052 Homo sapi
2	23856	79.7	180648	9	AP003043 Homo sapi
3	5698	19.6	160345	2	AC067870 Homo sapi
4	5610	18.7	160345	2	AC067870 Homo sapi
5	762	2.5	1149	9	AK025378 Homo sapi
6	652	2.2	1587	6	AX164746 Sequence
7	652	2.2	1734	6	AX164761 Sequence
8	652	2.2	1828	6	AX164744 Sequence
9	652	2.2	1828	9	AF335584 Homo sapi
10	652	2.2	3718	6	AX365307 Sequence
11	652	2.2	3736	6	AX365305 Sequence
12	652	2.2	4070	9	BC030645 Homo sapi
13	601	2.0	2253	9	AF336376 Homo sapi
14	550	1.8	3710	9	AY027518 Homo sapi
15	550	1.8	3729	9	AY027517 Homo sapi
16	460	1.5	485	6	AX331460 Sequence
17	377	1.3	1882	6	AX044487 Sequence
18	377	1.3	1882	6	AX207483 Sequence
19	236	0.8	1428	9	AB033832 Homo sapi
20	221	0.7	1162	6	AX454728 Sequence
21	221	0.7	1162	6	AX464052 Sequence
22	221	0.7	1162	6	AX491206 Sequence
23	221	0.7	1404	6	AX365309 Sequence
24	221	0.7	1404	6	AX463715 Sequence
25	220	0.7	462	6	AX164752 Sequence
26	220	0.7	199386	9	AC117440 Homo sapi
27	220	0.7	228137	2	AC117483 Homo sapi
28	190	0.6	173386	9	AC084781 Homo sapi
29	190	0.6	209779	9	AC066616 Homo sapi
30	185	0.6	156633	2	AC113431 Homo sapi
31	174	0.6	193404	2	AC103693 Homo sapi
32	174	0.6	213564	2	AC091030 Homo sapi
33	173	0.6	81374	9	HSJ300H18
34	172	0.6	3337	9	HS181842 Homo sapien
35	172	0.6	3512	9	HSAC001014 Homo sapi
36	172	0.6	3512	9	HMAC001014 Homo sapien
37	172	0.6	76819	9	AC004043 Homo sapi
38	172	0.6	83072	9	AL356793 Human DNA
39	172	0.6	116685	9	HS516C23 Human DNA s
40	172	0.6	168936	2	AC024992 Homo sapi
41	172	0.6	198586	9	AC079789 Homo sapi
42	170	0.6	170289	9	AC097648 Homo sapi
43	169	0.6	136495	9	AC005521 Homo sapi
44	168	0.6	3060	9	AB013905 Homo sapi
45	168	0.6	6091	9	HSDBRPE Homo sapiens

ALIGNMENTS

RESULT 1
AC024052
LOCUS
DEFINITION
AC024052
AC024052.3 GI:9838295
HTG; HTGS_PHASE1; HTGS_DRAFT
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 182403)
AUTHORS
Waterston,R.H.
TITLE
The sequence of Homo sapiens clone

AC024052 182403 bp DNA linear HTG 17-AUG-2000
Homo sapiens chromosome 11 clone RP11-617B3, WORKING DRAFT
SEQUENCE, 7 unordered pieces.

AC024052 182403 bp DNA linear HTG 17-AUG-2000
Homo sapiens chromosome 11 clone RP11-617B3, WORKING DRAFT
SEQUENCE, 7 unordered pieces.

Pred. No. is the number of results predicted by chance to have a

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unpublished
2 (bases 1 to 182403)
Waterston,R.H.
Direct Submission
Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:7109658.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Center project name: H.NH0617B03
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178574 bases at least Q40
Consensus quality: 179480 bases at least Q30
Consensus quality: 179940 bases at least Q20
Insert size: 198000; agarose-fp
Quality coverage: 5.39 in Q20 bases; agarose-fp
Quality coverage: 5.87 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1. 1666: contig of 1666 bp in length
1667 1766: gap of unknown length
1767 9133: contig of 7367 bp in length
9134 9233: gap of unknown length
9234 20663: contig of 11430 bp in length
20664 20763: gap of unknown length
20764 35927: contig of 15164 bp in length
35928 36028: gap of unknown length
36029 61610: contig of 25583 bp in length
61611 61710: gap of unknown length
61711 96167: contig of 34457 bp in length
96168 96267: gap of unknown length
96268 182403: contig of 86136 bp in length.

FEATURES

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20764. 35927
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misc_feature

96268. 182403
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misc_feature

clone_end:T

BASE COUNT 55923 a 35190 c 34519 g 56169 t 602 others
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 29921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	140075	TCGAGCAGGACCGACCTAATAGATATCTACAGAACTCCCAACCCCAATCAACAGATA	140134	Db	141155	AGGGAGTATGATGCCCTCAGCAAACTCTTAGGGCAGGACAGAACTAGCTTTGCCACAT	141214
QY	4021	TACACTCTTCTCAGCATCACAATACACCTTATTTAAATTTGACCATGTAAATTTAAGTAA	4080	QY	5101	TCGTATTCCAGATAAACAGATTTGCTGTTTGTATCAAGTAGCTCCAGTGGAAATGCTGAGT	5160
Db	140135	TACACTCTTCTCAGCATCACAATACACCTTATTTAAATTTGACCATGTAAATTTAAGTAA	140194	Db	141215	TCGTATTCCAGATAAACAGATTTGCTGTTTGTATCAAGTAGCTCCAGTGGAAATGCTGAGT	141274
QY	4081	AACTCTCTCAGAAATGCAAAAGAACAGAAATCTTACAAACAGTCTCTCAGACTACAG	4140	QY	5161	TGGTCATGATCCTTTGGCCTTTTGGCTCCCAAAACACATACACCTCTCAAGACTAAA	5220
Db	140195	AACTCTCTCAGAAATGCAAAAGAACAGAAATCTTACAAACAGTCTCTCAGACTACAG	140254	Db	141275	TGGTCATGATCCTTTGGCCTTTTGGCTCCCAAAACACATACACCTCTCAAGACTAAA	141334
QY	4141	TGCAATCTATTATAGAACTCAGAAATTAAGAACTCACTCAAAATCAACAACTACATGGAA	4200	QY	5221	CCAGAGAAAGTCAAAATCCCTGAATATACCACTAAACAGTTCTTAAATTTGAAGCAGTAAT	5280
Db	140255	TGCAATCTATTATAGAACTCAGAAATTAAGAACTCACTCAAAATCAACAACTACATGGAA	140314	Db	141335	CCAGAGAAAGTCAAAATCCCTGAATATACCACTAAACAGTTCTTAAATTTGAAGCAGTAAT	141394
QY	4201	ACTGAACACCTGCTCCTGAATGACTTACTGGTAAATACAAAATGAAGGCAAAAATAAA	4260	QY	5281	TGATAGCCTTACCAACCAAAAAAAGTCCAGGACAGACGGATTCACAGCCAAATTTTACCA	5340
Db	140315	ACTGAACACCTGCTCCTGAATGACTTACTGGTAAATACAAAATGAAGGCAAAAATAAA	140374	Db	141395	TGATAGCCTTACCAACCAAAAAAAGTCCAGGACAGACGGATTCACAGCCAAATTTTACCA	141454
				QY	5341	GAGGTACAAAGAGAGCTGGTACTATTCTTCTGAACTATTTCCTGAACTATTTCCTGAACTGAG	5400

QY	7561	ACACCATGAATACTATGACGCCATAAAAGAGTAGTTTCATGTCCTTTGCCAGAGATATG	7620	QY	8641	CAAGGCTGTCTGCTGCCCTCCCATGTAACCCGCGAGGAGACCTGTGATGCTTTGCTTGAA	8700
Db	143675	ACACCATGAATACTATGACGCCATAAAAGAGTAGTTTCATGTCCTTTGCCAGAGATATG	143734	Db	144755	CAAGGCTGTCTGCTGCCCTCCCATGTAACCCGCGAGGAGACCTGTGATGCTTTGCTTGAA	144814
QY	7621	GATGAAGCTGGAAACCATCATCTCTACGAAACTAACACAAGACACAGAAACCAACACCA	7680	QY	8701	CTTTTGTCTCAGGTGAAGTTAGATGCCCTGGAGTCCCTCGCACTCATGTCATCAGGTCCTG	8760
Db	143735	GATGAAGCTGGAAACCATCATCTCTACGAAACTAACACAAGACACAGAAACCAACACCA	143794	Db	144815	CTTTTGTCTCAGGTGAAGTTAGATGCCCTGGAGTCCCTCGCACTCATGTCATCAGGTCCTG	144874
QY	7681	CATGTTCTCAGTGAAGTGGAGTTGAACAATGAGAACACATGGACACAGGAGGGGAA	7740	QY	8761	CACATTCTCTCATTTAGAAATTTGCCATGCTTCCATAGACGGTCCAGTCCAGGCAGG	8820
Db	143795	CATGTTCTCAGTGAAGTGGAGTTGAACAATGAGAACACATGGACACAGGAGGGGAA	143854	Db	144875	CACATTCTCTCATTTAGAAATTTGCCATGCTTCCATAGACGGTCCAGTCCAGGCAGG	144934
QY	7741	CATCACACACAGGTCCTGTTGTGGTGGGACTAGGGAAGGGATAGCATTTAGAGAA	7800	QY	8821	AATAAATCACTCATTTGTTTAAATGTTCAATCAAGTTAGGCACTCTGCTGATGAGAAAT	8880
Db	143855	CATCACACACAGGTCCTGTTGTGGTGGGACTAGGGAAGGGATAGCATTTAGAGAA	143914	Db	144935	AATAAATCACTCATTTGTTTAAATGTTCAATCAAGTTAGGCACTCTGCTGATGAGAAAT	144994
QY	7801	ATACCTAAATGATGACGGGTGATGGTGCAGCAAGCCACATGGCACATGTATACCT	7860	QY	8881	GGAAGATGGAGATCTGTTTGTAGAAAACTTCAAAAGACTTCTCAAGTTCACAAAGTTGGCGAG	8940
Db	143915	ATACCTAAATGATGACGGGTGATGGTGCAGCAAGCCACATGGCACATGTATACCT	143974	Db	144995	GGAAGATGGAGATCTGTTTGTAGAAAACTTCAAAAGACTTCTCAAGTTCACAAAGTTGGCGAG	145054
QY	7861	ATGTAACAACCTGCACATCTGCACATGACCCACACACTTAAAGTATTAATAAAAAA	7920	QY	8941	GGGTTGGAGGAGGAATACCCCTAAGAAAGTCTTTAGGGAGACAAAGTCTCAGAAATTTT	9000
Db	143975	ATGTAACAACCTGCACATCTGCACATGACCCACACACTTAAAGTATTAATAAAAAA	144034	Db	145055	GGGTTGGAGGAGGAATACCCCTAAGAAAGTCTTTAGGGAGACAAAGTCTCAGAAATTTT	145114
QY	7921	CACACAACATGTTGCCCTGATGAAGGTCATTAGTGGCCATAAATAAGTAAAAATGTTTT	7980	QY	9001	GATTTGGTAAAGCTAGTCCAAAGCCAGTTTGTATGTTGATTTCTATTATCATCTCCTG	9060
Db	144035	CACACAACATGTTGCCCTGATGAAGGTCATTAGTGGCCATAAATAAGTAAAAATGTTTT	144094	Db	145115	GATTTGGTAAAGCTAGTCCAAAGCCAGTTTGTATGTTGATTTCTATTATCATCTCCTG	145174
QY	7981	ATGTTTTATATATTTGTTAAACATAAATATCTTTACCATTAAACAAATCAGGTGCC	8040	QY	9061	CAATTCTATGTCACATTACATAGGTACCTTGGAAAGGGTTGGGGTTTGACCTCCATAGC	9120
Db	144095	ATGTTTTATATATTTGTTAAACATAAATATCTTTACCATTAAACAAATCAGGTGCC	144154	Db	145175	CAATTCTATGTCACATTACATAGGTACCTTGGAAAGGGTTGGGGTTTGACCTCCATAGC	145234
QY	8041	ACTAAATCTTGTATATTAATACCTGTGATCAATACAGCATTTCTTAAATCAATAAGT	8100	QY	9121	TTTGGCAAGAATTTCTCAAGATGAATTAATGCTATTTCCTCAAGACTATCTGGCTGTA	9180
Db	144155	ACTAAATCTTGTATATTAATACCTGTGATCAATACAGCATTTCTTAAATCAATAAGT	144214	Db	145235	TTTGGCAAGAATTTCTCAAGATGAATTAATGCTATTTCCTCAAGACTATCTGGCTGTA	145294
QY	8101	ATATCATTAATTTTAAATTCATAAGTTTAAACATAAATTTCTTAAATAGTAGTTAAATA	8160	QY	9181	AAAGAGATTGAGAACTAGGGGATCAGGAGAGGAAATTAATTTCTAAAGAACTGAGCAT	9240
Db	144215	ATATCATTAATTTTAAATTCATAAGTTTAAACATAAATTTCTTAAATAGTAGTTAAATA	144274	Db	145295	AAAGAGATTGAGAACTAGGGGATCAGGAGAGGAAATTAATTTCTAAAGAACTGAGCAT	145354
QY	8161	GAAAGCAACCTTCTCCCTGCAGTGGCCCTTCATTTAGTGAATATTAGCTATTACATAG	8220	QY	9241	ATGATTAATATTCTCTTTTAAAGAACTGTTTATCAAGGCCATTAATTTCTGATGACT	9300
Db	144275	GAAAGCAACCTTCTCCCTGCAGTGGCCCTTCATTTAGTGAATATTAGCTATTACATAG	144334	Db	145355	ATGATTAATATTCTCTTTTAAAGAACTGTTTATCAAGGCCATTAATTTCTGATGACT	145414
QY	8221	ACATATACCTTGTAAATTTCCATCTCTGTTTCTTAATATACATAGTTCAGATTAATATT	8280	QY	9301	GGCAGCTGTAAATCAGAGCTTTGTCGATTTGTCGATTTGCTTTCTCATTTGAGGCAACAAAGTG	9360
Db	144335	ACATATACCTTGTAAATTTCCATCTCTGTTTCTTAATATACATAGTTCAGATTAATATT	144394	Db	145415	GGCAGCTGTAAATCAGAGCTTTGTCGATTTGTCGATTTGCTTTCTCATTTGAGGCAACAAAGTG	145474
QY	8281	ATTTACTTTTATCTTTAGATCCCGTTAGCCCTTTATTTTGGATTTTGTCCCATTTTCT	8340	QY	9361	TGTGCTTTGGGATAAGACAGAGCCTGGGCAAGTTTCTAACTGGTCTTCTGATGTTTC	9420
Db	144395	ATTTACTTTTATCTTTAGATCCCGTTAGCCCTTTATTTTGGATTTTGTCCCATTTTCT	144454	Db	145475	TGTGCTTTGGGATAAGACAGAGCCTGGGCAAGTTTCTAACTGGTCTTCTGATGTTTC	145534
QY	8341	TTTAGATTTAACTTGGTCATGGCACCAATTAACAAATTCATATAGCATTTTACAGTTT	8400	QY	9421	AGGGATTTTCTGTTGTTTTTATATTAAGCAAGCTGAGCACGGTATATATGTTTGTGCTG	9480
Db	144455	TTTAGATTTAACTTGGTCATGGCACCAATTAACAAATTCATATAGCATTTTACAGTTT	144514	Db	145535	AGGGATTTTCTGTTGTTTTTATATTAAGCAAGCTGAGCACGGTATATATGTTTGTGCTG	145594
QY	8401	GAAATTTTGCACAGGCACATTTTCTTTTCTTTTACCCCTCAGACAAATCTTTCACA	8460	QY	9481	ATAAGAAGAGAAAAATGAATGGCAGACACCTTTTCCAGACACACAGGAGGAGCAGCTAT	9540
Db	144515	GAAATTTTGCACAGGCACATTTTCTTTTCTTTTACCCCTCAGACAAATCTTTCACA	144574	Db	145595	ATAAGAAGAGAAAAATGAATGGCAGACACCTTTTCCAGACACACAGGAGGAGCAGCTAT	145654
QY	8461	TGGTGGAAAGGTATCATTTATCCCACTTTTACTGAGATTTCTAAAGGAGGATAAGTACC	8520	QY	9541	TTGAACAAAGTGGAAATTTGGACTGCTTACTGGATGATCAGACACTGATGTTCAAGCT	9600
Db	144575	TGGTGGAAAGGTATCATTTATCCCACTTTTACTGAGATTTCTAAAGGAGGATAAGTACC	144634	Db	145655	TTGAACAAAGTGGAAATTTGGACTGCTTACTGGATGATCAGACACTGATGTTCAAGCT	145714
QY	8521	TTGTCAGGGCTTCCCTGACTTGGACCTGGGACACAGGACCTGGGATCAGGACATTTAA	8580	QY	9601	TTGATCATGATTAATAGTCTTAGGTTTCAAGTACACAGCATTTCAAGAGGAGGAGAAAGCA	9660
Db	144635	TTGTCAGGGCTTCCCTGACTTGGACCTGGGACACAGGACCTGGGATCAGGACATTTAA	144694	Db	145715	TTGATCATGATTAATAGTCTTAGGTTTCAAGTACACAGCATTTCAAGAGGAGGAGAAAGCA	145774
QY	8581	GCTCTAGCATATCTGACTTTCAGGCTCTCTAACATGCTTCAATTTCTTTTATGCT	8640	QY	9661	GGCTGATTTGAGGGCATGTAGAAAAATGAAAAGCCCTTTTCTGAGAAAAGCAAACTGGCGG	9720
Db	144695	GCTCTAGCATATCTGACTTTCAGGCTCTCTAACATGCTTCAATTTCTTTTATGCT	144754	Db	145775	GGCTGATTTGAGGGCATGTAGAAAAATGAAAAGCCCTTTTCTGAGAAAAGCAAACTGGCGG	145834
				QY	9721	TTATAGGTTATCTGCTACCTTTTAAAGGAGGAGAACTGAATTAATATAGGAGCTGAA	9780

Db	146915	AGCAAAATATCTTTGAGAAGGGATAACATATATTTCTCCTCGAGTAATTACTCAACCT	146974
Qy	10861	GCAGGCAATATACACAGCTGGCTGGCATTTGTAAACAGAAGACGATGATATCAAGTCCCAA	10920
Db	146975	GCAGGCAATATACACAGCTGGCTGGCATTTGTAAACAGAAGACGATGATCAAGTCCCAA	147034
Qy	10921	GACACAGTACTAGTTAAAAAGACATAAATGACAAACAGCTCAACAGTGTATATTAAGA	10980
Db	147035	GACACAGTACTAGTTAAAAAGACATAAATGACAAACAGCTCAACAGTGTATATTAAGA	147094
Qy	10981	AGTTAAAGCTCAAGGTGACAAAAGCTGGGTATAGTGGGAGTTTATACATGCTCATGA	11040
Db	147095	AGTTAAAGCTGGAAGGTGACAAAAGCTGGGTATAGTGGGAGTTTATACATGCTCATGA	147154
Qy	11041	ATTTTGAANAATGCAATCATGATATCTGTGCGATATTTACTTCAAAATAGATGCGTCTGTGA	11100
Db	147155	ATTTTGAANAATGCAATCATGATATCTGTGCGATATTTACTTCAAAATAGATGCGTCTGTGA	147214
Qy	11101	GACTCTAGGGTTACTATGAGGTGTACTCAGTTGCGAGTTTAACTTTACAGAACTAAATAG	11160
Db	147215	GACTCTAGGGTTACTATGAGGTGTACTCAGTTGCGAGTTTAACTTTACAGAACTAAATAG	147274
Qy	11161	TTAAATGATTTTGACAGCACCTTAGAGGATTTAGAGATTTATGCTACATGTTTACGCTACCAATGCG	11220
Db	147275	TTAAATGATTTTGACAGCACCTTAGAGGATTTATGCTACATGTTTACGCTACCAATGCG	147334
Qy	11221	AGAAAACATAATGGAAGCCCTGGGTGGGCACCTACATTTTCAGAGCATGGCATTTAGCATTTGG	11280
Db	147335	AGAAAACATAATGGAAGCCCTGGGTGGGCACCTACATTTTCAGAGCATGGCATTTAGCATTTGG	147394
Qy	11281	GTATCACTCATGACACAGATGGGCGCTTGCTGCTTGGGGAGTACCTTGCCCATGTGGCA	11340
Db	147395	GTATCACTCATGACACAGATGGGCGCTTGCTGCTTGGGGAGTACCTTGCCCATGTGGCA	147454
Qy	11341	AGTTTGGCGCTTTGGCAGGAAGCCCTGATGTGAAGCTAGATTGAGAAGGGAGAAAGTGTG	11400
Db	147455	AGTTTGGCGCTTTGGCAGGAAGCCCTGATGTGAAGCTAGATTGAGAAGGGAGAAAGTGTG	147514
Qy	11401	CAGTTTGTAACTTTAAACAAGGAGTTCACATAACTTGTAAAGTGAGTCATCAGGGGAAGAA	11460
Db	147515	CAGTTTGTAACTTTAAACAAGGAGTTCACATAACTTGTAAAGTGAGTCATCAGGGGAAGAA	147574
Qy	11461	TGTAATCAGAACTGAGAAGCCAGACAGGCTCTCATCTAAATGCCACCACATCTGTCTTT	11520
Db	147575	TGTAATCAGAACTGAGAAGCCAGACAGGCTCTCATCTAAATGCCACCACATCTGTCTTT	147634
Qy	11521	GTACTTTATAGTCTTCAGATGCCCTTCATTCACCCAGTATCCCCAGGTGGTAGAAGCAC	11580
Db	147635	GTACTTTATAGTCTTCAGATGCCCTTCATTCACCCAGTATCCCCAGGTGGTAGAAGCAC	147694
Qy	11581	TGTCGTATCATTTGCCATTGTCGAAGATGAGTGAATTAACTTTTTTTAAAGCAGCTCATAAA	11640
Db	147695	TGTCGTATCATTTGCCATTGTCGAAGATGAGTGAATTAACTTTTTTTAAAGCAGCTCATAAA	147754
Qy	11641	CATTTACTGTTCTGGATCATATCTTTATTTCTTTTTTGCAATTTACCTAGCATTTCAACCACC	11700
Db	147755	CATTTACTGTTCTGGATCATATCTTTATTTCTTTTTTGCAATTTACCTAGCATTTCAACCACC	147814
Qy	11701	AATTTGTTTTTATTCCTTTACACAATTTCAATTAAGATTTTTGGGGCAGGATAAAGTGTAAAC	11760
Db	147815	AATTTGTTTTTATTCCTTTACACAATTTCAATTAAGATTTTTGGGGCAGGATAAAGTGTAAAC	147874
Qy	11761	AACAGATAAGTAATATGATGTAAATTTTCAGGTTTGCTCGGAACTCAAAATTTGATGTTAT	11820
Db	147875	AACAGATAAGTAATATGATGTAAATTTTCAGGTTTGCTCGGAACTCAAAATTTGATGTTAT	147934
Qy	11821	TATGGGATTAAGTGAGGAAACCTCAGGCCCTGGGAAGTTTTTAAAGTGGCTGGCTCTCAGT	11880
Db	147935	TATGGGATTAAGTGAGGAAACCTCAGGCCCTGGGAAGTTTTTAAAGTGGCTGGCTCTCAGT	147994
Qy	11881	TGCCCTTCCATGTGGCAAGCTGGAAACCAAGACCCACATCTTTTCTAGTCTGCAAGTTT	11940
Db	147995	TGCCCTTCCATGTGGCAAGCTGGAAACCAAGACCCACATCTTTTCTAGTCTGCAAGTTT	148054

QY	11941	TCTGCTCTATTTGGCCCTCTCTTGGTAGGAAACAACATCACAGACCATTGAGGCTTCACTTAAAG	12000
DB	148055	TCTGCTCTATTTGGCCCTCTCTTGGTAGGAAACAACATCACAGACCATTGAGGCTTCACTTAAAG	148114
QY	12001	GTCGAGAAAGCACAGAGGAGGACTCCACAGTTCTAGCTATGAGGTTTCCAAAAA	12060
DB	148115	GTCGAGAAAGCACAGAGGAGGACTCCACAGTTCTAGCTATGAGGTTTCCAAAAA	148174
QY	12061	AATAACAGAAAAGAGATTTTCTTGACCTTTTATTAATAGTTAGGTATATCATGACCCAAAA	12120
DB	148175	AATAACAGAAAAGAGATTTTCTTGACCTTTTATTAATAGTTAGGTATATCATGNCCCCAAA	148234
QY	12121	ACTCCCCTCCTATPCTGCTAGAGAGGAAAACCTCTTGGCGGAAATTTATTTCTGTTCTT	12180
DB	148235	ACTCCCCTCCTATPCTGCTAGAGAGGAAAACCTCTTGGCGGAAATTTATTTCTGTTCTT	148294
QY	12181	TGSGTCTCAATTTGAAAATTTAGTGACTTTTTTTTCAATACAGACGCTTTCAAACATGTAA	12240
DB	148295	TGSGTCTCAATTTGAAAATTTAGTGACTTTTTTTTCAATACAGACGCTTTCAAACATGTAA	148354
QY	12241	AAACAAAGTACTATTCTTTTACCTCAAACTGAAGGTCAACAGTGTATTACTCTAACCTC	12300
DB	148355	AAACAAAGTACTATTCTTTTACCTCAAACTGAAGGTCAACAGTGTATTACTCTAACCTC	148414
QY	12301	ATATTTTCATGTATAAATACAGATGCCTGTTGACTTATGATGGGGCTATATCTCTGATAAAC	12360
DB	148415	ATATTTTCATGTATAAATACAGATGCCTGTTGACTTATGATGGGGCTATATCTCTGATAAAC	148474
QY	12361	CCATTGGAGGTTAAANAATATTTTAAGTTGAAAATGCATTAATACCCCCCCCCATAACCCAC	12420
DB	148475	CCATTGGAGGTTAAANAATATTTTAAGTTGAAAATGCATTAATACCCCCCCCCATAACCCAC	148534
QY	12421	TGAAAAGTAAAAA AAAAAAAAAA TCTAACTAACCATCATTTAGAGTAATCTGTACCAAT	12480
DB	148535	TGAAAAGTAAAAA AAAAAAAAAA TCTAACTAACCATCATTTAGAGTAATCTGTACCAAT	148594
QY	12481	TTATTAATACATCTCTTAACCTTAACCTGTGATAAAAATGCAAAATGTTTAAATACAAAAT	12540
DB	148595	TTATTAATACATCTCTTAACCTTAACCTGTGATAAAAATGCAAAATGTTTAAATACAAAAT	148654
QY	12541	CTACCTTAGAACAGAGAGTCAATTTTTTTTTCATTTTGTCTAGATGCTTAAGTGATTTC	12600
DB	148655	CTACCTTAGAACAGAGAGTCAATTTTTTTTTCATTTTGTCTAGATGCTTAAGTGATTTC	148714
QY	12601	TAGATGCTATAAATGTGCCAGATCAGAGATAGGTATAGCTTGTGCCATTCAACAAGGT	12660
DB	148715	TAGATGCTATAAATGTGCCAGATCAGAGATAGGTATAGCTTGTGCCATTCAACAAGGT	148774
QY	12661	AGTCACGGCCTTGTGGGTAAATTTAAATTTCAATTTAGTTTAAACTAAATAAAATTA AAAA	12720
DB	148775	AGTCACGGCCTTGTGGGTAAATTTAAATTTCAATTTAGTTTAAACTAAATAAAATTA AAAA	148834
QY	12721	TTTAGTTTCTATTTGTGCTACACATTTCAAGTGGCCCAACAGCCACATGTTGCTAGTGA	12780
DB	148835	TTTAGTTTCTATTTGTGCTACACATTTCAAGTGGCCCAACAGCCACATGTTGCTAGTGA	148894
QY	12781	CTACCATATGGAACATTTGCAAAATATAGTTATTCCTATCACACAGAGAGATCTATTAGA	12840
DB	148895	CTACCATATGGAACATTTGCAAAATATAGTTATTCCTATCACACAGAGAGATCTATTAGA	148954
QY	12841	CAGTCAGGRTTGTAGTCAAGCATCTGAGAAAATTTATGAGGAGGAAGAACAGAGAAAT	12900
DB	148955	CAGTCAGGRTTGTAGTCAAGCATCTGAGAAAATTTATGAGGAGGAAGAACAGAGAAAT	149014
QY	12901	TACATCTATCTTATCTCTTTGATGCTTCTTATGTTTTTGGTGTGTGACTAAATGGATA	12960
DB	149015	TAACTATCTATCTTATCTCTTTGATGCTTCTTATGTTTTTGGTGTGTGACTAAATGGATA	149074
QY	12961	CAGCGGGCACC AAATCATGAAAACAGTTCAGTAATAATTTAATAGTCTACTACTT	13020
DB	149075	CAGCGGGCACC AAATCATGAAAACAGTTCAGTAATAATTTAATAGTCTACTACTT	149134
QY	13021	TTAGAAAATATCTCTCTTCAITATACACTATCAAGAGAGAGAACTGAAATATAGT	13080
DB	149135	TTAGAAAATATCTCTCTTCAITATACACTATCAAGAGAGAGAACTGAAATATAGT	149194
QY	13081	TTCCTCTAAATGTCTACAAATACGTTTTTCTGGAATCTCCCTTTTAACAAAATCACTA	13140
DB	149195	TTCCTCTAAATGTCTACAAATACGTTTTTCTGGAATCTCCCTTTTAACAAAATCACTA	149254
QY	13141	CCCAATATCTTTTATATCTATGATGGGTTTCTGAGACACTGTACTGCCCTTCCCTCAC	13200
DB	149255	CCCAATATCTTTTATATCTATGATGGGTTTCTGAGACACTGTACTGCCCTTCCCTCAC	149314
QY	13201	AGCTGAAGAAATTTGAGAAAACAAGAGAGAAAAGTACCTCTGACCTTCCCTCCCTCAC	13260
DB	149315	AGCTGAAGAAATTTGAGAAAACAAGAGAGAAAAGTACCTCTGACCTTCCCTCCCTCAC	149374
QY	13261	CTCCATCTCTGAAGAAAGTATATAAACCTAGGATTTTCTGACCTTCCCATGTACAGTCA	13320
DB	149375	CTCCATCTCTGAAGAAAGTATATAAACCTAGGATTTTCTGACCTTCCCATGTACAGTCA	149434
QY	13321	TAAAGACCTCATGCGAGAGGTGCCCTTGTATATCCAGAAAAGAAAGTATCCCTCCCTC	13380
DB	149435	TAAAGACCTCATGCGAGAGGTGCCCTTGTATATCCAGAAAAGAAAGTATCCCTCCCTC	149494
QY	13381	CCTTTTGTGTTGAGATGTGGTCTTACTCTGTCAACCCAGGCTAGAGTGCAGTGTGATGATC	13440
DB	149495	CCTTTTGTGTTGAGATGTGGTCTTACTCTGTCAACCCAGGCTAGAGTGCAGTGTGATGATC	149554
QY	13441	ATGTTCTGCTCAACCTTGACCTCTGGGCTCAAGCAATTTCTCTGCTCAGCTCCCTCCAA	13500
DB	149555	ATGTTCTGCTCAACCTTGACCTCTGGGCTCAAGCAATTTCTCTGCTCAGCTCCCTCCAA	149614
QY	13501	GTAGCTCAGACACAGACACATCTCCACACTTGGCTTACTTAAATAATTTCTTTT	13560
DB	149615	GTAGCTCAGACACAGACACATCTCCACACTTGGCTTACTTAAATAATTTCTTTT	149674
QY	13561	TATTAATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	13620
DB	149675	TATTAATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	149734
QY	13621	CTTGAACCTATAGCTCAAGGATCATCCACCTTGGCTTCAAGAGTGTGAGATTTACA	13680
DB	149735	CTTGAACCTATAGCTCAAGGATCATCCACCTTGGCTTCAAGAGTGTGAGATTTACA	149794
QY	13681	GGCATGAGCCACTCTCTCTGGCTTGAAGAATCTTATCTCAAAAGACAAAGGTAGAACAA	13740
DB	149795	GGCATGAGCCACTCTCTCTGGCTTGAAGAATCTTATCTCAAAAGACAAAGGTAGAACAA	149854
QY	13741	TAAGAACTGTGAACAAACAGGCTTGTCTAAATTTTCCCGAGTTTATTTACCATTAGATCATAC	13800
DB	149855	TAAGAACTGTGAACAAACAGGCTTGTCTAAATTTTCCCGAGTTTATTTACCATTAGATCATAC	149914
QY	13801	TCTGCCCTATCATATTTCTCCACAACTATCCACACTTTTATCAAACTTACTGTAAAAAAT	13860
DB	149915	TCTGCCCTATCATATTTCTCCACAACTATCCACACTTTTATCAAACTTACTGTAAAAAAT	149974
QY	13861	ATCAGGTTGAACCACTTTTTTTTGGTCTTCTCTTACCAAGGCTCTGTGCTCAGCTAAAAACAT	13920
DB	149975	ATCAGGTTGAACCACTTTTTTTGGTCTTCTCTTACCAAGGCTCTGTGCTCAGCTAAAAACAT	150034
QY	13921	ATTCAAATAAATGAGTACACTTTTCTTTTGTATATTCCTCTCTCTCTATATCTAGTATATTCC	13980
DB	150035	ATTCAAATAAATGAGTACACTTTTCTTTTGTATATTCCTCTCTCTCTATATCTAGTATATTCC	150094
QY	13981	CATGAACCTAGGAAGGTGGAAGAAAAGTATTTTTCTCTACTCTATATCTAGTATATTCC	14040
DB	150095	CATGAACCTAGGAAGGTGGAAGAAAAGTATTTTTCTCTACTCTATATCTAGTATATTCC	150154
QY	14041	AAGAAGCATAGAATGTTGTTTGAAGAGAGAAAATAACTTCAACAGGGTACCTTACAAAC	14100
DB	150155	AAGAAGCATAGAATGTTGTTTGAAGAGAGAAAATAACTTCAACAGGGTACCTTACAAAC	150214
QY	14101	TTTTGAGAGCAAGAAAATAAATAAGACAGTACACATTTTTTACTGACAGCTGAAAACCGCTCAA	14160

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Db	154595	TAATCAACATGTTAGAGAAAATGATTTTTTTGTGTGCAATATGGTGCATATTTCTGTGCAC	154654
Qy	18541	TGGTCTCTAGATGCGCAGTATAGCATAGTGGTTAAAGTGGTCTTGGAGCCGACGATAAAGTTAC	18600
Db	154655	TGGTCTCTAGATGCGCAGTATAGCATAGTGGTTAAAGTGGTCTTGGAGCCGACGATAAAGTTAC	154714
Qy	18601	AACGCGCTTCAATCACATCACATPAGGCTATGTTTCCCTTTTAGTTGGAAAGTTATTTAATGGCT	18660
Db	154715	AACGCGCTTCAATCACATCACATGCGCTATGTTTCCCTTTTAGTTGGAAAGTTATTTAATGGCT	154774
Qy	18661	CTGAACCTTCGCTTCCCTCATCTATAACATGTAATCATTTGAAGAAATTGAATGTAACGTGC	18720
Db	154775	CTGAACCTTCGCTTCCCTCATCTATAACATGTAATCATTTGAAGAAATTGAATGTAACGTGC	154834
Qy	18721	CTGCACTCAATGCCAGCTATCTTCTTACTAATCTTGATTTTCATCTGTAATCTCCCCCTCTCACA	18780
Db	154835	CTGCACTCAATGCCAGCTATCTTCTTACTAATCTTGATTTTCATCTGTAATCTCCCCCTCTCACA	154894
Qy	18781	TTCTTTTCCCTTTAAAGTCAAAATGGACAAAATTTAAAAATATACTACGCTTTTCTCCCTCT	18840
Db	154895	TTCTTTTCCCTTTAAAGTCAAAATGGACAAAATTTAAAAATATACTACGCTTTTCTCCCTCT	154954
Qy	18841	TTATGTTTTCTTCTTTGGCAATATATAAATGATTATCAAGGATATGGTCAGTGGGACT	18900
Db	154955	TTATGTTTTCTTCTTTGGCAATATATAAATGATTATCAAGGATATGGTCAGTGGGACT	155014
Qy	18901	TCATGAACATAAAGACCAACAATTTTCAAGCTAAGTCATATAATATTTACTTTGAATT	18960
Db	155015	TCATGAACATAAAGACCAACAATTTTCAAGCTAAGTCATATAATATTTACTTTGAATT	155074
Qy	18961	CAATTCGCATTTATGTGTACATAAATAGATTTGATTTTCGTGTTCTCCAAGTCCATCCA	19020
Db	155075	CAATTCGCATTTATGTGTACATAAATAGATTTGATTTTCGTGTTCTCCAAGTCCATCCA	155134
Qy	19021	ATTATCCATCCATTTGGCAGCCAATCCTCTATTATTGGTGCATACATGAGTATCTTC	19080
Db	155135	ATTATCCATCCATTTGGCAGCCAATCCTCTATTATTGGTGCATACATGAGTATCTTC	155194
Qy	19081	TCACAAGAACACAGTTAGAAGCAAGTCCTTTTGTCTGCACAGAACCCACCCCTTTCC	19140
Db	155195	TCACAAGAACACAGTTAGAAGCAAGTCCTTTTGTCTGCACAGAACCCACCCCTTTCC	155254
Qy	19141	AATGCACGCCCTTGTGTGCACAGGCCACCACAGAGAAATCCCATGAATGTTAGGCAGT	19200
Db	155255	AATGCACGCCCTTGTGTGCACAGGCCACCACAGAGAAATCCCATGAATGTTAGGCAGT	155314
Qy	19201	TATCACCATGTTCAATCTTAAACTCTAGCCCTGGTAAATGCTTTAGGCTTTAAACTGAACT	19260
Db	155315	TATCACCATGTTCAATCTTAAACTCTAGCCCTGGTAAATGCTTTAGGCTTTAAACTGAACT	155374
Qy	19261	GCTTAAAGGAGAAGGAAGAAAAAGCCTTTGGGAGCAGAGTCAAAAGTCAAGGACAGTG	19320
Db	155375	GCTTAAAGGAGAAGGAAGAAAAAGCCTTTGGGAGCAGAGTCAAAAGTCAAGGACAGTG	155434
Qy	19321	TCAGTAGAATGCATCTAAGGAAAAATTGCAGGAACAAAGTGTGGACCATGAGTCCACTAAC	19380
Db	155435	TCAGTAGAATGCATCTAAGGAAAAATTGCAGGAACAAAGTGTGGACCATGAGTCCACTAAC	155494
Qy	19381	GCATCCCTGTTGTCTTTTATATATCTACAATCTGCTTTGATCTCAAGGGCAGGGAATTT	19440
Db	155495	GCATCCCTGTTGTCTTTTATATATCTACAATCTGCTTTGATCTCAAGGGCAGGGAATTT	155554
Qy	19441	ATCCCCAATGTCATACGCTGAGCCCAAGGATACGTGGGAACATAAATAAGTCCCAATAA	19500
Db	155555	ATCCCCAATGTCATACGCTGAGCCCAAGGATACGTGGGAACATAAATAAGTCCCAATAA	155614
Qy	19501	TCAGTGTGCATAATTTATGCTGTTTTTTTCTCTTTGTTAAAGACATGTCTATACTTTA	19560
Db	155615	TCAGTGTGCATAATTTATGCTGTTTTTTTCTCTTTGTTAAAGACATGTCTATACTTTA	155674
Qy	19561	GCTATAATCAATCCAGATTTAAATGTAATGAACTCTGCTTTGGGAAAGCAACCATTTAT	19620

Db	155675	GCTATPAACTCAATCCAGATTTAAATTTGAATGAACCTCTGCTTGGGAAGGAACCAATTTTAT	155737
QY	19621	TGCTGCTAAAGCCCTGAAAATAAATCTGCAAGCAAAAGCAGAAAGGATTTACATAAATGGATT	19680
Db	155735	TGCTGCTAAAGCCCTGAAAATAAATCTGCAAGCAAAAGCAGAAAGGATTTACATAAATGGATT	155794
QY	19681	AGAAGTGCAGCAATCATCCATTTACAAGTGTCACCTTTGAGATAAAATCTGCTGCTTGCCCTG	19740
Db	155795	AGAAGTGCAGCAATCATCCATTTACAAGTGTCACCTTTGAGATAAAATCTGCTGCTTGCCCTG	155854
QY	19741	TGCATTCCTGGCTTGTGAACAGGGCTGATGCAGAGGGCCCAATCTGCTGCTTGCGATAA	19800
Db	155855	TGCATTCCTGGCTTGTGAACAGGGCTGATGCAGAGGGCCCAATCTGCTGCTTGCGATAA	155914
QY	19801	TGGGAAGATATTTTGCTTAACACGGAGGACTAAAGAGGTACAAATAGCAGGAAGGATCGT	19860
Db	155915	TGGGAAGATATTTTGCTTAACACGGAGGACTAAAGAGGTACAAATAGCAGGAAGGATCGT	155974
QY	19861	GATGTGTGAGAAGGCAGAGAGGACGAGGACGCAAGCGCAACACTGAGTCTCTGCTTTCCG	19920
Db	155975	GATGTGTGAGAAGGCAGAGAGGACGAGGACGCAAGCGCAACACTGAGTCTCTGCTTTCCG	156034
QY	19921	TTACAGCCCTCTGCTGAACATATGTCATACCTTTACAGATATGACTACATTTAGTTGTTCC	19980
Db	156035	TTACAGCCCTCTGCTGAACATATGTCATACCTTTACAGATATGACTACATTTAGTTGTTCC	156094
QY	19981	CACCCATTTCAAGTCAGTATTTATTTGCTTAAGAGTTTAAACAGTAAATGGTAAAACTGGAAAT	20040
Db	156095	CACCCATTTCAAGTCAGTATTTATTTGCTTAAGAGTTTAAACAGTAAATGGTAAAACTGGAAAT	156154
QY	20041	GAAAGCTTTCCGCCCTTTTGCTCCATPAGTCTCTGTCACCTTTTAAGCAGAATPAGAGGATGCT	20100
Db	156155	GAAAGCTTTCCGCCCTTTTGCTCCATPAGTCTCTGTCACCTTTTAAGCAGAATPAGAGGATGCT	156214
QY	20101	CAGTAAGCCATTAGTTGAAGNAGAAGACCAGTGTATGAGGGCTGTACTGACATTTCT	20160
Db	156215	CAGTAAGCCATTAGTTGAAGNAGAAGACCAGTGTATGAGGGCTGTACTGACATTTCT	156274
QY	20161	GTCTGATCTTGAACACAGGGTTGGGTGGTGAATGGCCACATCCTTATCTTCAGAAAGACAC	20220
Db	156275	GTCTGATCTTGAACACAGGGTTGGGTGGTGAATGGCCACATCCTTATCTTCAGAAAGACAC	156334
QY	20221	CAAGCCAAAGTACAGCATGCCCTCCCTATAGGAATTCCAATAACTCCAAAGTGCCCTCC	20280
Db	156335	CAAGCCAAAGTACAGCATGCCCTCCCTATAGGAATTCCAATAACTCCAAAGTGCCCTCC	156394
QY	20281	ACAAACACAGGAAGGCATGAAGCCCTCATCTCTATTGAAACCAACTCCTCACATTTGTA	20340
Db	156395	ACAAACACAGGAAGGCATGAAGCCCTCATCTCTATTGAAACCAACTCCTCACATTTGTA	156454
QY	20341	TAACCTCTTTGACTAGCATTTGTTACTTTTCATTTCTTACTCACCATGAGGAGATTCACAAT	20400
Db	156455	TAACCTCTTTGACTAGCATTTGTTACTTTTCATTTCTTACTCACCATGAGGAGATTCACAAT	156514
QY	20401	TCTGTCAAGTTTTATGCATCAATTTCACTAATGTCACTAAGAAGTGTGACCTGTGACTG	20460
Db	156515	TCTGTCAAGTTTTATGCATCAATTTCACTAATGTCACTAAGAAGTGTGACCTGTGACTG	156574
QY	20461	CTGTAGAATCAACCTGCCCTACATATCAGGCGATTTGAAATCACCGAGGCACATTTAG	20520
Db	156575	CTGTAGAATCAACCTGCCCTACATATCAGGCGATTTGAAATCACCGAGGCACATTTAG	156634
QY	20521	AATTAGAAGTCAAGAGGTTGTTCTGTGACTGGATGCCAATAACTTCAAGCGGTGATTCAGAC	20580
Db	156635	AATTAGAAGTCAAGAGGTTGTTCTGTGACTGGATGCCAATAACTTCAAGCGGTGATTCAGAC	156694
QY	20581	TTTCTGCAAGGGATATTGAGTTTCCAGTCAAAAGAGACTGTAAAGCCAGTGCAGCAGAGC	20640
Db	156695	TTTCTGCAAGGGATATTGAGTTTCCAGTCAAAAGAGACTGTAAAGCCAGTGCAGCAGAGC	156754
QY	20641	AGGAGCCAGACAGAGGCTGAGCAATTAAGAGTTTCTGTTGCTTTGGTTTGAAGGAGA	20700
Db	156755	AGGAGCCAGACAGAGGCTGAGCAATTAAGAGTTTCTGTTGCTTTGGTTTGAAGGAGA	156814

Qy	20701	ATTCAGAGTGAGACTTCTGGGAGGAGACAGCCAAAGTGGTCAACCAGAGAGAGGG	20760
Db	156815	ATTCAGAGTGAGACTTCTGGGAGGAGAGACAGCCAAAGTGGTCAACCAGAGAGAGGG	156874
Qy	20761	GCTGGCCCTTCTGTTCTCGATCAGTCTCCATAGCTGAACATTCAGAGCATCAAGGGTGT	20820
Db	156875	GCTGGCCCTTCTGTTCTCGATCAGTCTCCATAGCTGAACATTCAGAGCATCAAGGGTGT	156934
Qy	20821	TCCAATTTAAATCAAAGGCCGCTAAATTTCAACTAAAGCTCCCTTATTTTCATCCCAGTCT	20880
Db	156935	TCCAATTTAAATCAAAGGCCGCTAAATTTCAACTAAAGCTCCCTTATTTTCATCCCAGTCT	156994
Qy	20881	ACATCATGGAATAATCCCTCTTTTCTGTCATCTCGAATTTTAGTCTTTTATCAAAG	20940
Db	156995	ACATCATGGAATAATCCCTCTTTTCTGTCATCTCGAATTTTAGTCTTTTATCAAAG	157054
Qy	20941	CTCTTTGACATCAATTAAGTTTTTTGGGCTCATACAGGCAGTTTTCTGGAAGGCTGGG	21000
Db	157055	CTCTTTGACATCAATTAAGTTTTTTGGGCTCATACAGGCAGTTTTCTGGAAGGCTGGG	157114
Qy	21001	AAGGCTCCCCGCTCAAAAATCTCTTTTGACATACATGSTAAAGTGGGGCTGCTGCA	21060
Db	157115	AAGGCTCCCCGCTCAAAAATCTCTTTTGACATACATGSTAAAGTGGGGCTGCTGCA	157174
Qy	21061	CAGTGACAGGGGCGCACCTTTCTCTCGAGCCCTGCTCTAGGTGACGCCATAATCACA	21120
Db	157175	CAGTGACAGGGGCGCACCTTTCTCTCGAGCCCTGCTCTAGGTGACGCCATAATCACA	157234
Qy	21121	GAGGTGTTTGAGATGTAATAAGAATGCTGGGATCTGAGCTCTAGAATGGGGATGTGAAT	21180
Db	157235	GAGGTGTTTGAGATGTAATAAGAATGCTGGGATCTGAGCTCTAGAATGGGGATGTGAAT	157294
Qy	21181	GCACACCTTTTATAGTTTCTAATATATAGGTGGGAGGAGAGTCAACCTGTTCTT	21240
Db	157295	GCACACCTTTTATAGTTTCTAATATATAGGTGGGAGGAGAGTCAACCTGTTCTT	157354
Qy	21241	TTTGATCCTGGCCATCTAGACTACTAAGTCTGTGTTTCATCATGAGTGCATAAATCTC	21300
Db	157355	TTTGATCCTGGCCATCTAGACTACTAAGTCTGTGTTTCATCATGAGTGCATAAATCTC	157414
Qy	21301	ATAAATGCTATGAATTTACATACAATCATTTACTTCTTACTTTTGAGTGGAGAACTGAGC	21360
Db	157415	ATAAATGCTATGAATTTACATACAATCATTTACTTCTTACTTTTGAGTGGAGAACTGAGC	157474
Qy	21361	CTTTCAAAGTTTAAGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANA	21420
Db	157475	CTTTCAAAGTTTAAGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANA	157534
Qy	21421	GTAGAGCAGAGTTTGAATCCAGGCTCTTCATGCTTTGTGATATATGAGCCCAAGTGT	21480
Db	157535	GTAGAGCAGAGTTTGAATCCAGGCTCTTCATGCTTTGTGATATATGAGCCCAAGTGT	157594
Qy	21481	AAAGATTTGAAGAGGGTTTCAGAGCAGCTTCCACAGCGATGCTGAAGTCTTCCCACC	21540
Db	157595	AAAGATTTGAAGAGGGTTTCAGAGCAGCTTCCACAGCGATGCTGAAGTCTTCCCACC	157654
Qy	21541	AGAGGACCCTTGTGTGCAATGACCTGGCTTCTAGGTGACCCCATAGGCACHTAACCT	21600
Db	157655	AGAGGACCCTTGTGTGCAATGACCTGGCTTCTAGGTGACCCCATAGGCACHTAACCT	157714
Qy	21601	GTCAATTTTCAATGTCATTAATACACATFACCAAGCAGCAGCAGCTGTGTATCCTCATC	21660
Db	157715	GTCAATTTTCAATGTCATTAATACACATFACCAAGCAGCAGCAGCTGTGTATCCTCATC	157774
Qy	21661	CACCTATTCAGTTCTGACTTAATAAACCCAGGCAGCTATTCAGAGTCTACTTTTGTCTTGG	21720
Db	157775	CACCTATTCAGTTCTGACTTAATAAACCCAGGCAGCTATTCAGAGTCTACTTTTGTCTTGG	157834
Qy	21721	TATTTGATTAACAATTTGCTCTTTTATCTGAACCGAGTGACCTTTGGCCAAATGCACAC	21780
Db	157835	TATTTGATTAACAATTTGCTCTTTTATCTGAACCGAGTGACCTTTGGCCAAATGCACAC	157894
Qy	21781	TCCTCTTTTGTCTCTCAITTTCTCTCTGAACCCCTTTCTTGCCCTCATCTAGAGCTGAATGG	21844
Db	157895	TCCTCTTTTGTCTCTCAITTTCTCTCTGAACCCCTTTCTTGCCCTCATCTAGAGCTGAATGG	157954
Qy	21841	ATTGATAGCAATGATTTGTCTCTCAGTGGGBAACAANTGCCAGGATCCTAAAGATTC TAGTT	21900
Db	157955	ATTGATAGCAATGATTTGTCTCTCAGTGGGBAACAANTAAGGATCCTAAAGATTC TAGTT	158014
Qy	21901	TCTGTAGGACAGATAAAACCAATATAATTTTCCACATACCTTGCCAAAGCACAACATGGGTG	21960
Db	158015	TCTGTAGGACAGATAAAACCAATATAATTTTCCACATACCTTGCCAAAGCACAACATGGGTG	158074
Qy	21961	GTGATCAGCTTAAAGATAAAAAATTTAAATAATCTATCTTATTTAAAGTGAAACATAATTTAT	22020
Db	158075	GTGATCAGCTTAAAGATAAAAAATTTAAATAATCTATCTTATTTAAAGTGAAACATAATTTAT	158134
Qy	22021	TATTTTATACAAGTTACCTGTTCTGTTGGGACAGAAAGTCAAAATGTGCTTACTGGGTCAA	22080
Db	158135	TATTTTATACAAGTTACCTGTTCTGTTGGGACAGAAAGTCAAAATGTGCTTACTGGGTCAA	158194
Qy	22081	AATCAAGGATGTAAGAGTTAAGTCTGTTTTTGTGAATACAAAAATTCATTATGAAACAAA	22140
Db	158195	AATCAAGGATGTAAGAGTTAAGTCTGTTTTTGTGAATACAAAAATTCATTATGAAACAAA	158254
Qy	22141	ATAATCTCCTCACCTTTGAACATGGGAAAGCACCTTTGTTCTCCACATGCACATAATTTTA	22200
Db	158255	ATAATCTCCTCACCTTTGAACATGGGAAAGCACCTTTGTTCTCCACATGCACATAATTTTA	158314
Qy	22201	CTGCTTCTTTTGGTCAACAAGAGATGGTTTCTCTGAGTCAGTCTCTAAACATTTAAGTTA	22260
Db	158315	CTGCTTCTTTTGGTCAACAAGAGATGGTTTCTCTGAGTCAGTCTCTAAACATTTAAGTTA	158374
Qy	22261	TCAGTTGCGCTTTCAGTCTGCTGCCATTCATCAATCTTTATCTGATAGTAGAATCAGAT	22320
Db	158375	TCAGTTGCGCTTTCAGTCTGCTGCCATTCATCAATCTTTATCTGATAGTAGAATCAGAT	158434
Qy	22321	GCITTTTTCTCTTGATCATCCACAGACTGTGACAGAGAAATCAAATTAACCTGTCATGTCC	22380
Db	158435	GCITTTTTCTCTTGATCATCCACAGACTGTGACAGAGAAATCAAATTAACCTGTCATGTCC	158494
Qy	22381	TTGAAGACAGTCAGTAACTCTTTTCTCTTTTCTTTTCTTTTGTGACAGAGCTCT	22440
Db	158495	TTGAAGACAGTCAGTAACTCTTTTCTCTTTTCTTTTCTTTTGTGACAGAGCTCT	158554
Qy	22441	GCCTGCTGCCAGGCTGGAGTGCAGTGGCATGTTTCAAGTCACCATTAACCTTCCGCCCTC	22500
Db	158555	GCCTGCTGCCAGGCTGGAGTGCAGTGGCATGTTTCAAGTCACCATTAACCTTCCGCCCTC	158614
Qy	22501	CCAGTTTAAAGCAATTTCTCCGCCCTCAGCCTCTGAGTAGTGGGACTACAGGTGTGTCG	22560
Db	158615	CCAGTTTAAAGCAATTTCTCCGCCCTCAGCCTCTGAGTAGTGGGACTACAGGTGTGTCG	158674
Qy	22561	CACATGCCCAGCTAAATTTTGTATTTTCATTTAGAGATAGAGTTTCAACATGTTGGCACCA	22620
Db	158675	CACATGCCCAGCTAAATTTTGTATTTTCATTTAGAGATAGAGTTTCAACATGTTGGCACCA	158734
Qy	22621	GTAATCATTTTATTTGTTGTACAAAGCTTAGCCCTTATATGCTAAAGTCTTTTATAAAC	22680
Db	158735	GTAATCATTTTATTTGTTGTACAAAGCTTAGCCCTTATATGCTAAAGTCTTTTATAAAC	158794
Qy	22681	TCATTAGCAGGCATGCAGCAGCCCTACATACCTAGTGTGCATTTTACCACATGGTGTATGGC	22740
Db	158795	TCATTAGCAGGCATGCAGCAGCCCTACATACCTAGTGTGCATTTTACCACATGGTGTATGGC	158854
Qy	22741	ATGTGGAGAAATGAGCACTCAAAAGTAGGCCATGATGTTTTTGAACACCATGCTCTTGTTC	22800
Db	158855	ATGTGGAGAAATGAGCACTCAAAAGTAGGCCATGATGTTTTTGAACACCATGCTCTTGTTC	158914
Qy	22801	TTCTGTTTCTCTTCTGCGCATCTCAGCTTGCTATATTTTATCTTCTTAGAGCTCA	22860
Db	158915	TTCTGTTTCTCTTCTGCGCATCTCAGCTTGCTATATTTTATCTTCTTAGAGCTCA	158974
Qy	22861	AGTCAAAAAGGCATATTCACCTCTACATCTCCTATGACTCTCTCTATGACTCACCACAC	22920

QY	25081	AATCCTACCTCTCAGTAGGTATGCCACATTTACTGAAGTGAGTAACACAGATCAAAAG	25140	26161	CCCTCATAGACACACACAAATATGATAAAACAATATGTTTTTATGATGCTTGTCTGCG	26220
Db	161195	AATCCTACCTCTCAGTAGGTATGCCACATTTACTGAAGTGAGTAACACAGATCAAAAG	161254	162275	CCCTCATAGACACACACAAATATGATAAAACAATATGTTTTTATGATGCTTGTCTGCG	162334
QY	25141	AAGGAAGTTTAAATCAGAAAGCACCTAAACACTAGAAGGAGCTGAGATTCGTAAATGGTGA	25200	26221	AAACAGAGTAGTGAGGAGCTAGATCTTACAAATCATATGAGTCATAAACAGTGGCAA	26280
Db	161255	AAGGAAGTTTAAATCAGAAAGCACCTAAACACTAGAAGGAGCTGAGATTCGTAAATGGTGA	161314	162335	AAACAGAGTAGTGAGGAGCTAGATCTTACAAATCATATGAGTCATAAACAGTGGCAA	162394
QY	25201	TTACTAAGGAATAGAGGCCATGCCACCTTGAACCTAAATACAAAAGCCATGATCAGG	25260	26281	AAGTCTCTAAAAGAAAAGCTTAGCAGAAAACATCCCAATAGCAAAATAGTGTGAGAAA	26340
Db	161315	TTACTAAGGAATAGAGGCCATGCCACCTTGAACCTAAATACAAAAGCCATGATCAGG	161374	162395	AAGTCTCTAAAAGAAAAGCTTAGCAGAAAACATCCCAATAGCAAAATAGTGTGAGAAA	162454
QY	25261	TGCTCTCAGTTTGAATACATCAGAGCTAACACTATCTCTTGGCAAGTGATTAAGTCCATTC	25320	26341	ATTTCTGGATAAATAGTATCAGAAAAGTTTAGTACTTGGAGATAATTTTGAACACTTTTA	26400
Db	161375	TGCTCTCAGTTTGAATACATCAGAGCTAACACTATCTCTTGGCAAGTGATTAAGTCCATTC	161434	162455	ATTTCTGGATAAATAGTATCAGAAAAGTTTAGTACTTGGAGATAATTTTGAACACTTTTA	162514
QY	25321	TCATCTAGATTAAGAAACACCCCAAGACTGGGTAGTTTATAAGAAAAGAGTTTAATG	25380	26401	ATGAGTACACTGATTTACAGATAATTAATAAGACAATATTTGCCAATACTACTCTGTG	26460
Db	161435	TCATCTAGATTAAGAAACACCCCAAGACTGGGTAGTTTATAAGAAAAGAGTTTAATG	161494	162515	ATGAGTACACTGATTTACAGATAATTAATAAGACAATATTTGCCAATACTACTCTGTG	162574
QY	25381	GCCTCACAGTTATGATTCGCTGGAGGCGCTAAGCAACTTACAACTATGCCAGAGGCG	25440	26461	AGGCTCTCCAGATTACTGATGTTTATCTTAGAGCCTTATAGGAAAGACAGCAGACAAT	26520
Db	161495	GCCTCACAGTTATGATTCGCTGGAGGCGCTAAGCAACTTACAACTATGCCAGAGGCG	161554	162575	AGGCTCTCCAGATTACTGATGTTTATCTTAGAGCCTTATAGGAAAGACAGCAGACAAT	162634
QY	25441	AAGGAAGCAAAAGCAGCTCTTACATGGTGCAGGAGGAGAGCATGTGTGCAAGTGTA	25500	26521	AATAGAAATATCTTGGTCTGTGCAGAGTTTTCAGCAANTTCAAAATATACAGTAGCT	26580
Db	161555	AAGGAAGCAAAAGCAGCTCTTACATGGTGCAGGAGGAGAGCATGTGTGCAAGTGTA	161614	162635	AATAGAAATATCTTGGTCTGTGCAGAGTTTTCAGCAANTTCAAAATATACAGTAGCT	162694
QY	25501	GGGGAACCTGCCCTTTATAAATCATCAGATCTGTGCCACTCAGTATACACAAGAT	25560	26581	ATCATTTATGAGGCTGTAGATCTCTTCAATACCTTAATCCCTAACCAAAATTTGCAAA	26640
Db	161615	GGGGAACCTGCCCTTTATAAATCATCAGATCTGTGCCACTCAGTATACACAAGAT	161674	162695	ATCATTTATGAGGCTGTAGATCTCTTCAATACCTTAATCCCTAACCAAAATTTGCAAA	162754
QY	25561	AGCATGGGAAACCATCCCATGATTCAAATATCTCCATCTTGTCTCCCTTCACATG	25620	26641	GTGCTTATAAATTAGAGCCATTTTACAAAGAGAAGAAAATAGAGATCAGGGGTCTGTAG	26700
Db	161675	AGCATGGGAAACCATCCCATGATTCAAATATCTCCATCTTGTCTCCCTTCACATG	161734	162755	GTGCTTATAAATTAGAGCCATTTTACAAAGAGAAGAAAATAGAGATCAGGGGTCTGTAG	162814
QY	25621	TGGGATATGGGATTTGGGATTTGCAATTCAGATGAGATTTGGTGGGACACAAAT	25680	26701	TGACTTCTCCAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGAAATTTTATACAAAT	26760
Db	161735	TGGGATATGGGATTTGGGATTTGCAATTCAGATGAGATTTGGTGGGACACAAAT	161794	162815	TGACTTCTCCAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGAAATTTTATACAAAT	162874
QY	25681	GCATCACTATATTACAGATAAGACACTCAGTGTGATCTCTCAGCAGCAGCAGG	25740	26761	TAGTTTGACTCTCAAGTCCATGCTCTTCCATTCGCAAGCTCTTCTTCTTCTTCTCTAT	26820
Db	161795	GCATCACTATATTACAGATAAGACACTCAGTGTGATCTCTCAGCAGCAGCAGG	161854	162875	TAGTTTGACTCTCAAGTCCATGCTCTTCCATTCGCAAGCTCTTCTTCTTCTTCTCTAT	162934
QY	25741	CCTACAAGCATATAGCTCTAGGAGCAGTGTAGTCTCTTCAAGTCTAGTGGGSCATAA	25800	26821	TTCTATTAATTTATGCCCCAACAAATTTTAAATATGATAAATAAAACTTTTCACTTGGTAAA	26880
Db	161855	CCTACAAGCATATAGCTCTAGGAGCAGTGTAGTCTCTTCAAGTCTAGTGGGSCATAA	161914	162935	TTCTATTAATTTATGCCCCAACAAATTTTAAATATGATAAATAAAACTTTTCACTTGGTAAA	162994
QY	25801	AGGAAAACATCCCATATAATTTTCCAAATGCTTCACAGAAAAAATTAGCACACAAC	25860	26881	GGTACCAATATACCAATGCTTCAGGAACTCAATGAAGCTAACCATCTTTCAATAATA	26940
Db	161915	AGGAAAACATCCCATATAATTTTCCAAATGCTTCACAGAAAAAATTAGCACACAAC	161974	162995	GGTACCAATATACCAATGCTTCAGGAACTCAATGAAGCTAACCATCTTTCAATAATA	163054
QY	25861	ACAAGGAACACATTTCTTTTAAAGAGTAATGAGTGGGAAAATGCAATTTGTC	25920	26941	GAACTATTATTAACAATAATGATATTAATAAGCAACACAGTTATTTATTAATGCTCTA	27000
Db	161975	ACAAGGAACACATTTCTTTTAAAGAGTAATGAGTGGGAAAATGCAATTTGTC	162034	163055	GAACTATTATTAACAATAATGATATTAATAAGCAACACAGTTATTTATTAATGCTCTA	163114
QY	25921	ATCCGACGCTAAAGCTTACCTATGCTTCCACTGTCAACTGGATTTTCTTATTTGATTT	25980	27001	TTATCTACTGATGTACCAGTACCTCTTAAATTTACAGAGATGTAGTTTACAGATATCTGA	27060
Db	162035	ATCCGACGCTAAAGCTTACCTATGCTTCCACTGTCAACTGGATTTTCTTATTTGATTT	162094	163115	TTATCTACTGATGTACCAGTACCTCTTAAATTTACAGAGATGTAGTTTACAGATATCTGA	163174
QY	25981	GCATTTGAATGACATGCTTAGATGAGGGGAATAACTTTGATAATGAGGTTGGGTTAGGA	26040	27061	AGACTGATGATCTGACTCATCTGCTGGCCACACAGCTTTTGGCAAAATCTTCAACC	27120
Db	162095	GCATTTGAATGACATGCTTAGATGAGGGGAATAACTTTGATAATGAGGTTGGGTTAGGA	162154	163175	AGACTGATGATCTGACTCATCTGCTGGCCACACAGCTTTTGGCAAAATCTTCAACC	163234
QY	26041	TATCCACAAACGACAACTGCGTCTAGGATGAAGCAGAGGTGGCAGCAGCAGGA	26100	27121	CAAGTATCAATAGCAGACAGAAAAATTCGACAGCTCAGTTTCTAAATAATGCTTCAT	27180
Db	162155	TATCCACAAACGACAACTGCGTCTAGGATGAAGCAGAGGTGGCAGCAGCAGGA	162214	163235	CAAGTATCAATAGCAGACAGAAAAATTCGACAGCTCAGTTTCTAAATAATGCTTCAT	163294
QY	26101	GGAAAAACACTGAAAGTTGCCACTGCTGAGATTTTCTTAAATAATTTTCAATGCTGTG	26160	27181	ATGTTAATGCTCTCTGAAATAATTTCTTACATTTGAAATCAATTTTGAATAATCAAACTT	27240
Db	162215	GGAAAAACACTGAAAGTTGCCACTGCTGAGATTTTCTTAAATAATTTTCAATGCTGTG	162274	163295	ATGTTAATGCTCTCTGAAATAATTTCTTACATTTGAAATCAATTTTGAATAATCAAACTT	163354
				27241	GTGCTCTCTCTTGTAGCATGCGGATGACAAAGAACAGCAATAATGATATAAATTT	27300


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QY 29461 GTCCGAATGGATTGCTGGGTTTTCTTCTAGGATTTTATGGTTTAGGTCTAACATT 29520
|||||
Db 16575 GTCCGAATGGATTGCTGGGTTTTCTTCTAGGATTTTATGGTTTAGGTCTAACATT 165634
|||||
QY 29521 TAAGTCTTTAATCCATCTTGAATTAATTTTGTATAAGGTGAAGGAAGGATCCAGTTT 29580
|||||
Db 165635 TAAGTCTTTAATCCATCTTGAATTAATTTTGTATAAGGTGAAGGAAGGATCCAGTTT 165694
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QY 29581 CAGCTTTCTACATAGGGCTAGCCAGTTTCTCAGCACCATTTATTAAATAGGAATCCCT 29640
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Db 165695 CAGCTTTCTACATAGGGCTAGCCAGTTTCTCAGCACCATTTATTAAATAGGAATCCCT 165754
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QY 29641 TCCCATTTGCTTTTCTCAGGTTTGTCAAGATCAGATAGTTGTAGATATGCGGCAT 29700
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Db 165755 TCCCATTTGCTTTTCTCAGGTTTGTCAAGATCAGATAGTTGTAGATATGCGGCAT 165814
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ACCESSION AP003043
VERSION AP003043.2 GI:15637094
KEYWORDS HTG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2000)
REFERENCE 2 (bases 1 to 180648)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) Masahira Hattori, The Institute of Physical
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(E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Sep 17, 2001 this sequence version replaced gi:11862945.
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DB	45923	ATAAGCAACTTCAGCAAGTCTCAGGACACAAAATCAATGTGCAAAAATCACAAGCAATC	45982	DB	47002	TTTATGAGCCCAACAAACATATGAAAAACCTCATCATCTGTTGTTAGAAAATGC	47061
QY	6116	TTATACGCCAATATACACAAACAGAGAGCAAAATCATGAGTGAACCTCATTCACAAAT	6175	QY	7195	AAAACAAACACAGTGCACATACCATCTCATGCTAGTTAGATGCTGATCACTAAAAGT	7254
DB	45983	TTATACGCCAATATACACAAACAGAGAGCAAAATCATGAGTGAACCTCATTCACAAAT	46042	DB	47062	AAAACAAACACAGTGCACATACCATCTCATGCTAGTTAGATGCTGATCACTAAAAGT	47121
QY	6176	GCTACAAAGAGAAATAACCTAGGAATACAACTTACAAAGGACAGCTAGGAACCTCTC	6235	QY	7255	CAGAAACAAACAAATGCTGGAGAGGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGT	7314
DB	46043	GCTACAAAGAGAAATAACCTAGGAATACAACTTACAAAGGACAGCTAGGAACCTCTC	46102	DB	47122	CAGAAACAAACAAATGCTGGAGAGGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGT	47181
QY	6236	AAGGAGAACTACAAACCACTGATCAAGGAAATAGAGAGGACACAAACAAATGAAAAAC	6295	QY	7315	GGGAATGTAATTTAGTTCAACCATTTGGAGACAGTGTGGAGATTCCTTAAGGATCTAG	7374
DB	46103	AAGGAGAACTACAAACCACTGATCAAGGAAATAGAGAGGACACAAACAAATGAAAAAC	46162	DB	47182	GGGAATGTAATTTAGTTCAACCATTTGGAGACAGTGTGGAGATTCCTTAAGGATCTAG	47241
QY	6296	ATTCATGCTCACAGATAGTAAGAAATCATGAAAT-GCCATACCTGCCCAAGTAAATAT	6354	QY	7375	AACCAGAAATATCAATTTGACCCAGCAATCCCATCTAGTATATACCCAAAGGAATATA	7434
DB	46163	ATTCATGCTCACAGATAGTAAGAAATCATGAAATGGCCATCTGCCCAAGTAAATAT	46222	DB	47242	AACCAGAAATATCAATTTGACCCAGCAATCCCATCTAGTATATACCCAAAGGAATATA	47301
QY	6355	AGATTGAGTGTACCCCTCATCAGCTACCAATGACTTTCTTCACAGAAATTTGAAAAACA	6414	QY	7435	AATCATCTTATTAATAAGACACATGCACATATGTTTATTTGACGACTGATCAACAATAG	7494
DB	46223	AGATTGAGTGTACCCCTCATCAGCTACCAATGACTTTCTTCACAGAAATTTGAAAAACA	46282	DB	47302	AATCATCTTATTAATAAGACACATGCACATATGTTTATTTGACGACTGATCAACAATAG	47361
QY	6415	ACTTTAAATTTTCATATGGACCAAAAAAGAGCCACAGAGCCCAAGCAATCTTAAGCAA	6474	QY	7495	CAAGACTTTGGAACCAACCCCAATGTCATCAGTATAGACTGATTAAGAAACATAGGC	7554
DB	46283	ACTTTAAATTTTCATATGGACCAAAAAAGAGCCACAGAGCCCAAGCAATCTTAAGCAA	46342	DB	47362	CAAGACTTTGGAACCAACCCCAATGTCATCAGTATAGACTGATTAAGAAACATAGGC	47421
QY	6475	AAAGAACAAAGCTGGAGGTATCATGCTACCTGACTTAAACTATATAGGCTACAGT	6534	QY	7555	ACATATACCATCAATTAATCTATGCAGCCATAAAAAAGGATGAGTTCTCTTTGCGAGA	7614
DB	46343	AAAGAACAAAGCTGGAGGTATCATGCTACCTGACTTAAACTATATAGGCTACAGT	46402	DB	47422	ACATATACCATCAATTAATCTATGCAGCCATAAAAAAGGATGAGTTCTCTTTGCGAGA	47481
				QY	7615	GATATGATGAAGCTGGAAACCAATCATTTCTCAGCAAACTAACACAGAACAGAAACCAA	7674

Db	47482	GATATGATGAAGCTGGAACCATCATCTCAGCAAACTAAACAAGAACAGAAAACCCA	47541	Db	48562	CTTGAACTTTTGTCTAGGTGAAAGTTAGATGCCTGGAGTCCCTCCACTCATGCATCAC	48621
QY	7675	ACACCACATGTTCTCACTTGTAGTGGAGTTCGAACAATGAGAAGACATGGACACAGGGA	7734	QY	8755	GGTCTGCACATCCCTTTTCATTTAGAAATTTGGCATGCTCTTCATAGACGGTCCAGTGAG	8814
Db	47542	ACACCACATGTTCTCACTTGTAGTGGAGTTCGAACAATGAGAAGACATGGACACAGGGA	47601	Db	48622	GGTCTGCACATCCCTTTTCATTTAGAAATTTGGCATGCTCTTCATAGACGGTCCAGTGAG	48681
QY	7735	GGGGAACATCACACACAGGTCCTGTTTGTGGTGGGACTAGGGAAGGATAGCATTA	7794	QY	8815	GCAGGGAATPAATCACTGCATTTGTTTAAATGTTCAATCAAGTTAGGGCACTCTGCTGATG	8874
Db	47602	GGGGAACATCACACACAGGTCCTGTTTGTGGTGGGACTAGGGAAGGATAGCATTA	47661	Db	48682	GCAGGGAATPAATCACTGCATTTGTTTAAATGTTCAATCAAGTTAGGGCACTCTGCTGATG	48741
QY	7795	GGAGAATACCTAATAGATGACGGTGTGATGGGTGCAGCAAGCCACCATGGCAGATGT	7854	QY	8875	CAGAAATGGAAGATGGAGATCTCTTGTAGAAAACCTTCAAAAACCTTGTGAGGAGACAAAGT	8934
Db	47662	GGAGAATACCTAATAGATGACGGTGTGATGGGTGCAGCAAGCCACCATGGCAGATGT	47721	Db	48742	CAGAAATGGAAGATGGAGATCTCTTGTAGAAAACCTTCAAAAACCTTGTGAGGAGACAAAGT	48801
QY	7855	ATACCTATGTAAACAACTGCACATTTGCACATGTACCCCAACCTTAAAGTATTAAAA	7914	QY	8935	TGCGAGGGGTGGAGGAAGAAATACCTTAAGAAAGTTCTTTAGGAGACAAAGTGTGAGA	8994
Db	47722	ATACCTATGTAAACAACTGCACATTTGCACATGTACCCCAACCTTAAAGTATTAAAA	47781	Db	48802	TGCGAGGGGTGGAGGAAGAAATACCTTAAGAAAGTTCTTTAGGAGACAAAGTGTGAGA	48861
QY	7915	AAAAACACACACATGTTGCCCTGATGAAGTTCATTTAGTGGCCATPAATAAGTAAATG	7974	QY	8995	AATTTTGAATATTGGTAAAGCTAGTCCAAAGCCAGTTTGTAGATGTTGATTTCTATTATCAT	9054
Db	47782	AAAAACACACACATGTTGCCCTGATGAAGTTCATTTAGTGGCCATPAATAAGTAAATG	47841	Db	48862	AATTTTGAATATTGGTAAAGCTAGTCCAAAGCCAGTTTGTAGATGTTGATTTCTATTATCAT	48921
QY	7975	TGTTTTATGTTTTATATATTGTTAAACATATAATATCCTTTACCATTAAAGTAAATG	8034	QY	9055	CTCCTGCAATTTCTATTGCACATTTACATAGTACCTTGGAGGGTGGGGTTTGGACTCC	9114
Db	47842	TGTTTTATGTTTTATATATTGTTAAACATATAATATCCTTTACCATTAAAGTAAATG	47901	Db	48922	CTCCTGCAATTTCTATTGCACATTTACATAGTACCTTGGAGGGTGGGGTTTGGACTCC	48981
QY	8035	GGTTCCACATAAATCTTGTATTAATACCTGTGTATCAATACAGCATTTCTTAAATCA	8094	QY	9115	CATAGCTTGGCAAGAATTTCTCCAAGATGAATTAATTCCTATTTTCCAAAGACTATCTGG	9174
Db	47902	GGTTCCACATAAATCTTGTATTAATACCTGTGTATCAATACAGCATTTCTTAAATCA	47961	Db	48982	CATAGCTTGGCAAGAATTTCTCCAAGATGAATTAATTCCTATTTTCCAAAGACTATCTGG	49041
QY	8095	ATAAGTATATCATTAATTTTAAATTCATAAGTTTAAACATAATTTCTTAAATTAGTAGT	8154	QY	9175	CCTGTAAAAGAGATTTGAGAATAGGGGATGAGGAGAGGGAAATTTTCTTAAAGAACT	9234
Db	47962	ATAAGTATATCATTAATTTTAAATTCATAAGTTTAAACATAATTTCTTAAATTAGTAGT	48021	Db	49042	CCTGTAAAAGAGATTTGAGAATAGGGGATGAGGAGAGGGAAATTTTCTTAAAGAACT	49101
QY	8155	TAAATAGAGCCAAACCTTCTCCCTGCAGTGGCCTTCATTTAGTGAATATATTAGCTATT	8214	QY	9235	GAGCATATGATTAATATTCCTTGTTTAAAGAGACTGTTTATCAAGCCCTAAATATTGTTG	9294
Db	48022	TAAATAGAGCCAAACCTTCTCCCTGCAGTGGCCTTCATTTAGTGAATATATTAGCTATT	48081	Db	49102	GAGCATATGATTAATATTCCTTGTTTAAAGAGACTGTTTATCAAGCCCTAAATATTGTTG	49161
QY	8215	ACATAGACATATCTTGTGTAATTCATTTCTTGTTCATATATACATAGTCAGATTA	8274	QY	9295	ATGACTGGCACCTGTAAATATCAGAGCTTGTGCTTGTCTCATTTTTCAGCGGCAACA	9354
Db	48082	ACATAGACATATCTTGTGTAATTCATTTCTTGTTCATATATACATAGTCAGATTA	48141	Db	49162	ATGACTGGCACCTGTAAATATCAGAGCTTGTGCTTGTCTCATTTTTCAGCGGCAACA	49221
QY	8275	TATATTATTACTTTATGTTCTTAGATCCCGTGTAGCCTTTATTTTGTGTTTGTCCCAT	8334	QY	9355	AAAGTGTGCTTTGGGATAAGCAAGAGCCCTGGGAGCTTTTCTTAACCTGCTTCTGA	9414
Db	48142	TATATTATTACTTTATGTTCTTAGATCCCGTGTAGCCTTTATTTTGTGTTTGTCCCAT	48201	Db	49222	AAAGTGTGCTTTGGGATAAGCAAGAGCCCTGGGAGCTTTTCTTAACCTGCTTCTGA	49281
QY	8335	TTTCCTTTTAGATTCTAAACTTGGTCATGGCACCATTAAACAATTCATAGCATTTTACA	8394	QY	9415	TTGTTTCAGGATTTCTCTGCTTTTATATTAAAGCAACGTGAGCGGTATATATGCTTT	9474
Db	48202	TTTCCTTTTAGATTCTAAACTTGGTCATGGCACCATTAAACAATTCATAGCATTTTACA	48261	Db	49282	TTGTTTCAGGATTTCTCTGCTTTTATATTAAAGCAACGTGAGCGGTATATATGCTTT	49341
QY	8395	GTTTTTGAATAATTTGCACAGGCACTATTTTCTTTTCTTTTACCCCTCAGACAAATCT	8454	QY	9475	TTGCTGATAAGAAAGAGAAAAATGAATTTGGCAGACACCTTTTCCAGACAGAGAGAG	9534
Db	48262	GTTTTTGAATAATTTGCACAGGCACTATTTTCTTTTCTTTTACCCCTCAGACAAATCT	48321	Db	49342	TTGCTGATAAGAAAGAGAAAAATGAATTTGGCAGACACCTTTTCCAGACAGAGAGAG	49401
QY	8455	TTACATGTTGGAAGATATCATATATGCCCCCTTTATATAGATTTCTTAAAGGAGGATA	8514	QY	9535	CACATTTTGAACAAAGTGGAAATTTGACTGCTTTACTGGATGATCACAGCCTGATGTTTC	9594
Db	48322	TTACATGTTGGAAGATATCATATATGCCCCCTTTATATAGATTTCTTAAAGGAGGATA	48381	Db	49402	CACATTTTGAACAAAGTGGAAATTTGACTGCTTTACTGGATGATCACAGCCTGATGTTTC	49461
QY	8515	AGTACCTTCCAGGGTCTTCCCTGACCTTGGACCTGGACAGGACCTGGGATCAGGAC	8574	QY	9595	AAAGCTTTCAGATCATGTAATAGTCTTAGGTTTCAGTACACAGCTTGAAGAAAGGAAGA	9654
Db	48382	AGTACCTTCCAGGGTCTTCCCTGACCTTGGACCTGGACAGGACCTGGGATCAGGAC	48441	Db	49462	AAAGCTTTCAGATCATGTAATAGTCTTAGGTTTCAGTACACAGCTTGAAGAAAGGAAGA	49521
QY	8575	ATTTAAGCTTCTAGCATATTTGACTTGGAGGCTCTCTAATCATGCTTCAATTTCTCTTT	8634	QY	9655	AAAGCTTTCAGATCATGTAATAGTCTTAGGTTTCAGTACACAGCTTGAAGAAAGGAAGA	9714
Db	48442	ATTTAAGCTTCTAGCATATTTGACTTGGAGGCTCTCTAATCATGCTTCAATTTCTCTTT	48501	Db	49522	AAAGCTTTCAGATCATGTAATAGTCTTAGGTTTCAGTACACAGCTTGAAGAAAGGAAGA	49581
QY	8635	ATGCTCAAGGTGTCTGGTCCCTCCCATGTGAACCCGAGGAGACCTGTGATGCTTTG	8694	QY	9715	TGGCGGTTATAGGTTATCTGGTCACCTTTAAAGGGAAGGAACACCTGAATTAATATAGA	9774
Db	48502	ATGCTCAAGGTGTCTGGTCCCTCCCATGTGAACCCGAGGAGACCTGTGATGCTTTG	48561	Db	49582	TGGCGGTTATAGGTTATCTGGTCACCTTTAAAGGGAAGGAACACCTGAATTAATATAGA	49641
QY	8695	CTTGAACTTTTCTCCTAGGTGAAGTTAGATGCTTGGAGTCCCTTGCATCATGATCAC	8754	QY	9775	GCTGAAGGCACTTCTTAATAGGTACCTTCACACAACTTTCTTTATTTTCTGAGCTATG	9834
				Db	49642	GCTGAAGGCACTTCTTAATAGGTACCTTCACACAACTTTCTTTATTTTCTGAGCTATG	49701

Qy	9835	ATTACAGCTGGAAGCACACAAACAGAAATAAATAATCCACTGGCGGCAACAGCATTT	9894	10913	AGTCCCAAGACACAGTACTCAGTTAAAAAGACATAATGACAAACAGCTCAACAGTGTTA	10972
Db	49702	ATTACAGCTGGAAGCACACACAGAAATAAATAATCCACTGGCGGCAACAGCATTT	49761	50782	AGTCCCAAGACACAGTACTCAGTTAAAAAGACATAATGACAAACAGCTCAACAGTGTTA	50841
Qy	9895	CTTAACACCTATGGTGCAAAATGGGGATCTTGACTCTCTCCACTCTGGAAACACACACA	9954	10973	TATTAAGAAGTTAAGCTTGAAGGTGACAAAAGCTGGGTATATAGTGGGAGTTTATAACAT	11032
Db	49762	CTTAACACCTATGGTGCAAAATGGGGATCTTGACTCTCTCCACTCTGGAAACACACACA	49821	50842	TATTAAGAAGTTAAGCTTGAAGGTGACAAAAGCTGGGTATATAGTGGGAGTTTATAACAT	50901
Qy	9955	AAGCAGGGAACCTTGACGCTACTAAATGAGTGTGACATGACCAATCTGGTGGTTCA	10014	11033	GCTCATGAATTTTGAANAATGCAATCATGATATCTGTCATATTTACTTCAAAATAGATGCG	11092
Db	49822	AAGCAGGGAACCTTGACGCTACTAAATGAGTGTGACATGACCAATCTGGTGGTTCA	49881	50902	GCTCATGAATTTTGAANAATGCAATCATGATATCTGTCATATTTACTTCAAAATAGATGCG	50961
Qy	10015	TACCACCATCAAAATCAAAAGATGCTCAGTTTTCGAAATTTACCTCATCAAAAAGATATT	10074	11093	TTCTGTGAGACTCTAGGGTTTACTATGAGGTGTACTCAGTTGCGAGTTTAACTTTACAGAA	11152
Db	49882	TACCACCATCAAAATCAAAAGATGCTCAGTTTTCGAAATTTACCTCATCAAAAAGATATT	49941	50962	TTCTGTGAGACTCTAGGGTTTACTATGAGGTGTACTCAGTTGCGAGTTTAACTTTACAGAA	51021
Qy	10075	TAACTACAGTTACTCAGCTTGTGGCCAAATAAGCTCTGGAATTAATCTCACCATAAAGCT	10134	11153	CTAAATAGTTAAATGATTTTGACAGCACTTACAGGATTAATGACTACATGTTTCAGGCTA	11212
Db	49942	TAACTACAGTTACTCAGCTTGTGGCCAAATAAGCTCTGGAATTAATCTCACCATAAAGCT	50001	51022	CTAAATAGTTAAATGATTTTGACAGCACTTACAGGATTAATGACTACATGTTTCAGGCTA	51081
Qy	10135	ATTACACTAATAAAACAATACAGGCAGAAAAGCTATCTGCTGAGTCTGGTCTGTTT	10194	11213	CCAATTCAGAAAACATAAATGGAAGGCTGGGTGGGCACATACATTTTCAGAGCATGGCATTT	11272
Db	50002	ATTACACTAATAAAACAATACAGGCAGAAAAGCTATCTGCTGAGTCTGGTCTGTTT	50061	51082	CCAATTCAGAAAACATAAATGGAAGGCTGGGTGGGCACATACATTTTCAGAGCATGGCATTT	51141
Qy	10195	ATTGAGAAATAAAAAAGGCTGTAAAG-CTTTGTAACAGTTTCTCAAATTAATGGCTGAC	10253	11273	AGCATTTGGGTATCAGTATGACACAGATGGGCCCTTGTCTCTTGGGAGTAGCTTGCCCC	11332
Db	50062	ATTGAGAAATAAAAAAGGCTGTAAAGGCTTGTAAAGCTTCTCAAATTAATGGCTGAC	50121	51142	AGCATTTGGGTATCAGTATGACACAGATGGGCCCTTGTCTCTTGGGAGTAGCTTGCCCC	51201
Qy	10254	TTAGGAACACAGTACGTATTTTACAGGACAAATGATTAATAACCCAAATCATTAAGAG	10313	11333	ATGTGGCAAGTTTGCCTTTTGGCAGGAAGGCTGATGTGAAGTAGATTTGAGAAGGGAG	11392
Db	50122	TTAGGAACACAGTACGTATTTTACAGGACAAATGATTAATAACCCAAATCATTAAGAG	50181	51202	ATGTGGCAAGTTTGCCTTTTGGCAGGAAGGCTGATGTGAAGTAGATTTGAGAAGGGAG	51261
Qy	10314	TTTAAGATCTCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCAGTCTCTTG	10373	11393	AAGGTGTGCAGTTTGTAAATCTTAAACAAGGAGTTCCTAACTTGTAAAGTGAGTCAATCAG	11452
Db	50182	TTTAAGATCTCTCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCAGTCTCTTG	50241	51262	AAGGTGTGCAGTTTGTAAATCTTAAACAAGGAGTTCCTAACTTGTAAAGTGAGTCAATCAG	51321
Qy	10374	CCAGGCTAGAGTGCAATGGTGTATCCCGGGTCACTGCAACCTTCCACCTCCCGGGTTCA	10433	11453	GGAGAAATTAATCAGAACTGAGAACCCAGCAGCCAGGCTCTCATCTAAATTTCCACCCACA	11512
Db	50242	CCAGGCTAGAGTGCAATGGTGTATCCCGGGTCACTGCAACCTTCCACCTCCCGGGTTCA	50301	51322	GGAGAAATTAATCAGAACTGAGAACCCAGCAGCCAGGCTCTCATCTAAATTTCCACCCACA	51381
Qy	10434	AGTGATCTCGCTCAGCTCCCAAGTAGCTGGGACTACAGGACAGTCCGACAGGCC	10493	11513	TCGTCTTGTACITTTATAGTCTTCAGATGCTTCAATTCACCCAGTATCCCCAGGTGTAA	11572
Db	50302	AGTGATCTCGCTCAGCTCCCAAGTAGCTGGGACTACAGGACAGTCCGACAGGCC	50361	51382	TCGTCTTGTACITTTATAGTCTTCAGATGCTTCAATTCACCCAGTATCCCCAGGTGTAA	51441
Qy	10494	TGGCTAATTTTGTATTTTAGTAGAGAT- GGGTTTCCACAGTTGSCCAGGCTGGTCTT	10552	11573	GAAGCACATCTGTATCATTTGCTCAAGTAGTGAATTAACCTTTTATTAAGCAG	11632
Db	50362	TGGCTAATTTTGTATTTTAGTAGAGATGGGTTTCCACAGTTGSCCAGGCTGGTCTT	50421	51442	GAAGCACATCTGTATCATTTGCTCAAGTAGTGAATTAACCTTTTATTAAGCAG	51501
Qy	10553	GAACCTCTGACCTCAGTGATCTGCCCTCAGCCTCCCAAAATGCTGGGATTTACAGGC	10612	11633	TCATAAACATTTACTCTCTGGATCATATCTTTATTTCTTTTGTGCAATTTACCTAGCATTT	11692
Db	50422	GAACCTCTGACCTCAGTGATCTGCCCTCAGCCTCCCAAAATGCTGGGATTTACAGGC	50481	51502	TCATAAACATTTACTCTCTGGATCATATCTTTATTTCTTTTGTGCAATTTACCTAGCATTT	51561
Qy	10613	ATGAGGACATCTGGCCCGGCTCTCTTCCAACTTCAAAACAGGCTGTTTTCAGCACACACA	10672	11693	CAACCACCAATTTGTTTTTATTCCTTACACAAATTTTAAAGATTTTGGGGCAGGATAA	11752
Db	50482	ATGAGGACATCTGGCCCGGCTCTCTTCCAACTTCAAAACAGGCTGTTTTCAGCACACACA	50541	51562	CAACCACCAATTTGTTTTTATTCCTTACACAAATTTTAAAGATTTTGGGGCAGGATAA	51621
Qy	10673	GTTCCTCAAGGAAAAAAGCTTCTCTTTTGATCTCTTTCATGCTTATAGCCTTTATA	10732	11753	AGTGTAAACAACAGATAATGAATGATGTAATTTTCAGGTTTGCCTGGGAACTCAAAATTG	11812
Db	50542	GTTCCTCAAGGAAAAAAGCTTCTCTTTTGATCTCTTTCATGCTTATAGCCTTTATA	50601	51622	AGTGTAAACAACAGATAATGAATGATGTAATTTTCAGGTTTGCCTGGGAACTCAAAATTG	51681
Qy	10733	AAAAATGTACACAGAGTCAATATTTTAAAGGATGCTAGTGAATTTCTGAAACCTTAAG	10792	11813	TAGGTATTTATGGGGATTAAGTGAAGAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGG	11872
Db	50602	AAAAATGTACACAGAGTCAATATTTTAAAGGATGCTAGTGAATTTCTGAAACCTTAAG	50661	51682	TAGGTATTTATGGGGATTAAGTGAAGAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGG	51741
Qy	10793	TGACTACAAGCAAAATATCTTGAGAAAGGATACATATTTTTCCTCCCTGAGTAATTA	10852	11873	TCCTCAGTTGCCCTTCATGTGGCAAGCTGGAAACCCAGACCCACATCTTTTCTAGTCCT	11932
Db	50662	TGACTACAAGCAAAATATCTTGAGAAAGGATACATATTTTTCCTCCCTGAGTAATTA	50721	51742	TCCTCAGTTGCCCTTCATGTGGCAAGCTGGAAACCCAGACCCACATCTTTTCTAGTCCT	51801
Qy	10853	CTCAACCTGACGCAATAATCAGACAGTGGCTGGCATTTGTAACAGAGGACTGATATCA	10912	11933	GCAAGTTTCTGCTCTATTTGCCCTCTCTTGGTAGAAAAACATCACACACCATGAGGCTTC	11992
Db	50722	CTCAACCTGACGCAATAATCAGACAGTGGCTGGCATTTGTAACAGAGGACTGATATCA	50781	51802	GCAAGTTTCTGCTCTATTTGCCCTCTCTTGGTAGAAAAACATCACACACCATGAGGCTTC	51861
				11993	ACTTAAAGGTGGAGAAAGGACAGAGGCGCAGAGACTCCACAAAGTTCTAGCTATGAGGTT	12052

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52942	DB	ATAATAGTGTCTCTAAATGCTACACAATACAGCTTTTCTGGAATCCTCCCTTTAACAAA	53001
13133	QY	AATCACTACCCAAATATCTTTTATATCTCTATGATGGGTTCTCAGGACACTGTACTCCCAA	13192
53002	DB	AATCACTACCCAAATATCTTTTATATCTCTATGATGGGTTCTCAGGACACTGTACTCCCAA	53061
13193	QY	ATGTTTAAAGCTGAAGGAATTTGAGAAACACAGAAAGCAGAAAGATCACTCTGACCTTC	13252
53062	DB	ATGTTTAAAGCTGAAGGAATTTGAGAAACACAGAAAGCAGAAAGATCACTCTGACCTTC	53121
13253	QY	CCCTCACCTCCATCTCTGAAGGAAGTCATAAAACCTAGGATTTCTGACCTTCCCATGTA	13312
53122	DB	CCCTCACCTCCATCTCTGAAGGAAGTCATAAAACCTAGGATTTCTGACCTTCCCATGTA	53181
13313	QY	GCAAGTCATAAGACCCCTCATGCGAGAGGTGCCCTGTTATACCCAGAGAAAGAAATTT	13372
53182	DB	GCAAGTCATAAGACCCCTCATGCGAGAGGTGCCCTGTTATACCCAGAGAAAGAAATTT	53241
13373	QY	CCCCCGCCCTTTTGTGTTGAGATGTGCTTACTCTGTCACCCAGGCTAGAGTCAGTT	13432
53242	DB	CCCCCGCCCTTTTGTGTTGAGATGTGCTTACTCTGTCACCCAGGCTAGAGTCAGTT	53301
13433	QY	GCATGATCATGTTCTGCTGCAACCTTTGAACCTCTGGGCTCAAGCAATTTCTCGCTCAG	13492
53302	DB	GCATGATCATGTTCTGCTGCAACCTTTGAACCTCTGGGCTCAAGCAATTTCTCGCTCAG	53361
13493	QY	CTCCCAAGTAGCTCAGACCACAGACATCTCTCCACACTTGGCTACTTAAANAATAATTC	13552
53362	DB	CTCCCAAGTAGCTCAGACCACAGACATCTCTCCACACTTGGCTACTTAAANAATAATTC	53421
13553	QY	CTTTTTTTTATTTATTTATTTATTTTATTTTATGAGATGGGGGCTCGCTATGTTGACC	13612
53422	DB	CTTTTTTTTATTTATTTATTTATTTTATGAGATGGGGGCTCGCTATGTTGACC	53481
13613	QY	CGGTTGATCTGAACCTATAGCCTCAAGGGATCATCCACCTTGGCTCTCAAGTGTGTG	13672
53482	DB	CGGTTGATCTGAACCTATAGCCTCAAGGGATCATCCACCTTGGCTCTCAAGTGTGTG	53541
13673	QY	AGATTACAGCATGAGCCACTGCTCTGGCCTAAGAACTCCTTATCTCAAAGACAAAAGT	13732
53542	DB	AGATTACAGCATGAGCCACTGCTCTGGCCTAAGAACTCCTTATCTCAAAGACAAAAGT	53601
13733	QY	AGAACAAATAAGAAATCTGAACAAACAGGCGTTGCTAAATTTTCCCGAGTTTATTTACCATTA	13792
53602	DB	AGAACAAATAAGAAATCTGAACAAACAGGCGTTGCTAAATTTTCCCGAGTTTATTTACCATTA	53661
13793	QY	GATCATACTCGCCCTATCATATTTCTCCACAACTATCCACACTTTTATCAAACTTACTGT	13852
53662	DB	GATCATACTCGCCCTATCATATTTCTCCACAACTATCCACACTTTTATCAAACTTACTGT	53721
13853	QY	AAAAAATATCAGGTTGAACCACTTTTGGTGCTTCTCTTACCAAGGCTCTGTGTACG	13912
53722	DB	AAAAAATATCAGGTTGAACCACTTTTGGTGCTTCTCTTACCAAGGCTCTGTGTACG	53781
13913	QY	TAAACATATTCATTAATGAGTACACTTTTCCCTTTGTTATTTCTCTTTTGTATTAGTG	13972
53782	DB	TAAACATATTCATTAATGAGTACACTTTTCCCTTTGTTATTTCTCTCTTTTGTATTAGTG	53841
13973	QY	GCCTCAGCATGAACCTAGGAAGGGTGAAGAAAAGGTATTTTCTACTCTATATCTPAG	14032
53842	DB	GCCTCAGCATGAACCTAGGAAGGGTGAAGAAAAGGTATTTTCTACTCTATATCTPAG	53901
14033	QY	TATATTTCCAAAGACATAGAATGATTTGTTTAGAAAGAGGAAAATFACITTCACAGGGTAC	14092
53902	DB	TATATTTCCAAAGACATAGAATGATTTGTTTAGAAAGAGGAAAATFACITTCACAGGGTAC	53961
14093	QY	CTCAAACTTTTGAGAGCAGAANAATAAAGACAGTCCACATTTTACTGACAGTGAAGA	14152
53962	DB	CTCAAACTTTTGAGAGCAGAANAATAAAGACAGTCCACATTTTACTGACAGTGAAGA	54021
14153	QY	CCGCTCAAAACCCCTACAGGACAACTAATATGACCTGTGAAAAGACAAATATTAGCTCGT	14212
54022	DB	CCGCTCAAAACCCCTACAGGACAACTAATATGACCTGTGAAAAGACAAATATTAGCTCGT	54081

Qy	18592	TAAAGTTACAACTGCCCTTCAATCACATCATGGGTATGTTTCCCTTTAGTTGGAAGTTAT	18651
Db	58460	TAAAGTTACAACTGCCCTTCAATCACATCATGGGTATGTTTCCCTTTAGTTGGAAGTTAT	58519
Qy	18652	TTAATGGCTCTGAACCTCTCTCCCTCATCATATAAAGATGAATGAAATGAAAT	18711
Db	58520	TTAATGGCTCTGAACCTCTCTCCCTCATCATATAAAGATGAATGAAATGAAAT	58579
Qy	18712	GTAACTGCTCT - GCACCTCAATGCCAGCTATCTTACTAACTTGAATTCATCTCAATCTCC	18770
Db	58580	GTAACTGCTCTGCCACTCAATGCCAGCTATCTTACTAACTTGAATTCATCTCAATCTCC	58639
Qy	18771	CCCTCTCACATCTCTTCCCTTTAAAGTCAAAATGGACAAAATTTAAATAATATCTACGTCT	18830
Db	58640	CCCTCTCACATCTCTTCCCTTTAAAGTCAAAATGGACAAAATTTAAATAATATCTACGTCT	58699
Qy	18831	TTCTCCCTCTTATGTTTCTCTTGGACATATATAAATGATTTCAAGGATATGTT	18890
Db	58700	TTCTCCCTCTTATGTTTCTCTTGGACATATATAAATGATTTCAAGGATATGTT	58759
Qy	18891	CAGTGGGACTCTATGAACATAAAGACCAACAATATTTTCAAGCTAAAGTCATAAATATT	18950
Db	58760	CAGTGGGACTCTATGAACATAAAGACCAACAATATTTTCAAGCTAAAGTCATAAATATT	58819
Qy	18951	TACTTGAATTCATATGCCATTTATGTTTACATAAATTAGATTTGATTTCTGCTCTCTCCA	19010
Db	58820	TACTTGAATTCATATGCCATTTATGTTTACATAAATTAGATTTGATTTCTGCTCTCTCCA	58879
Qy	19011	AGTCCATCCAAATTCATCCATTTGGCAGCCAAATCTCTTATTTGGTGCATCATACAT	19070
Db	58880	AGTCCATCCAAATTCATCCATTTGGCAGCCAAATCTCTTATTTGGTGCATCATACAT	58939
Qy	19071	GAGTATCTCTCAAGAACACACAGTTAGAGCAAGTCTCTTGTCTGCACAGAACCCACC	19130
Db	58940	GAGTATCTCTCAAGAACACACAGTTAGAGCAAGTCTCTTGTCTGCACAGAACCCACC	58999
Qy	19131	ACCCTTTCCCAATGCAGCCCTTGTGTGCACAGCCACACAGAGGAATCCCATGAAT	19190
Db	59000	ACCCTTTCCCAATGCAGCCCTTGTGTGCACAGCCACACAGAGGAATCCCATGAAT	59059
Qy	19191	GTTAGGCAATTCACATCTGTTTCAATCTAACTCTAGCCCTGTTAAATGCTTAGGCTTA	19250
Db	59060	GTTAGGCAATTCACATCTGTTTCAATCTAACTCTAGCCCTGTTAAATGCTTAGGCTTA	59119
Qy	19251	AACTGAACTGCTTAAAGCAAGCAAGAAAGAAAGCTTTGGGAGCAGAGGTCAAAAGTC	19310
Db	59120	AACTGAACTGCTTAAAGCAAGCAAGAAAGAAAGCTTTGGGAGCAGAGGTCAAAAGTC	59179
Qy	19311	AAGGACAGTGTAGTGAATGCATCTAAGGAAATTCAGGAAACAAAGTGTGGACCATGAG	19370
Db	59180	AAGGACAGTGTAGTGAATGCATCTAAGGAAATTCAGGAAACAAAGTGTGGACCATGAG	59239
Qy	19371	TCCACTAACCGCATCCCTGTTTGTCTTTTATCTACACTGTGCTTGTATCTCAAG	19430
Db	59240	TCCACTAACCGCATCCCTGTTTGTCTTTTATCTACACTGTGCTTGTATCTCAAG	59299
Qy	19431	GCAGGATTTATCCCAATTTGTCATACGCTGAGCCCAAGTACTGTGGGAACTAAATATA	19490
Db	59300	GCAGGATTTATCCCAATTTGTCATACGCTGAGCCCAAGTACTGTGGGAACTAAATATA	59359
Qy	19491	TGCCAAATATCACTGTGCATAATTTATGCTGTTTTTTTCTTCTTCTTCTTCTTCTTCT	19550
Db	59360	TGCCAAATATCACTGTGCATAATTTATGCTGTTTTTTTCTTCTTCTTCTTCTTCTTCT	59419
Qy	19551	CATAACTTTAGCTATATCAATCCAGATTTAAATGAACTGTCTTCTTCTTCTTCTTCTTCT	19610
Db	59420	CATAACTTTAGCTATATCAATCCAGATTTAAATGAACTGTCTTCTTCTTCTTCTTCTTCT	59479
Qy	19611	ACCATTTTATGCTGCTTAAAGCCCTGAAATAAATACTCAAGCAAGCAAGGATTTACAT	19670
Db	59480	ACCATTTTATGCTGCTTAAAGCCCTGAAATAAATACTCAAGCAAGCAAGGATTTACAT	59539

Qy	19671	AAATGGATTAAGAGTGCAGCAATCATCTCCATTTACAAGTGTCACTCTTGAGATAAATACTGA	19730
Db	59540	AAATGGATTAAGAGTGCAGCAATCATCTCCATTTACAAGTGTCACTCTTGAGATAAATACTGA	59599
Qy	19731	TGCTGGCTCTGATCTCCCTGGCTTGTGAACAGGGCTGTGACAGAGGCGCAAAATCTGCTG	19790
Db	59600	TGCTGGCTCTGATCTCCCTGGCTTGTGAACAGGGCTGTGACAGAGGCGCAAAATCTGCTG	59659
Qy	19791	CTTGTGATTAATGGAAAGATATTGTTCTAACACGGAGGACTTAAAGAGGTACAATTAGCAGG	19850
Db	59660	CTTGTGATTAATGGAAAGATATTGTTCTAACACGGAGGACTTAAAGAGGTACAATTAGCAGG	59719
Qy	19851	AAGGATCTGTGATGTGTGAAGAGGACAGAGAGGACAGGACGCAAGGCGCAAACTGAGTC	19910
Db	59720	AAGGATCTGTGATGTGTGAAGAGGACAGAGAGGACAGGACGCAAGGCGCAAACTGAGTC	59779
Qy	19911	TCCTGCTTCTGCTCAGCCCTCTGCTGAACTATGTCATAAACCCTTACAGATATGACTACATTT	19970
Db	59780	TCCTGCTTCTGCTCAGCCCTCTGCTGAACTATGTCATAAACCCTTACAGATATGACTACATTT	59839
Qy	19971	AGTTGTTCCCCACCCATTTCAAGTGAATTTATTTGCTAAGAGTTAACAGTAAATGGTAA	20030
Db	59840	AGTTGTTCCCCACCCATTTCAAGTGAATTTATTTGCTAAGAGTTAACAGTAAATGGTAA	59899
Qy	20031	AACTGGAATTAAGAGCTTTTCCCTTTTGTCTCCATAGTCTCTGTACTTTTAAAGCAGAATA	20090
Db	59900	AACTGGAATTAAGAGCTTTTCCCTTTTGTCTCCATAGTCTCTGTACTTTTAAAGCAGAATA	59959
Qy	20091	GAGGATGTCAGTAAGCCATTTAGTTGAAGGAGAGAGGACAGTGTATGAGGGCTGTACT	20150
Db	59960	GAGGATGTCAGTAAGCCATTTAGTTGAAGGAGAGAGGACAGTGTATGAGGGCTGTACT	60019
Qy	20151	GGACTTTCTGCTGATGTTGAACAGGCTTGGTGGTGAATGGCCACATCTTATCTTC	20210
Db	60020	GGACTTTCTGCTGATGTTGAACAGGCTTGGTGGTGAATGGCCACATCTTATCTTC	60079
Qy	20211	AGAAGACACCCAAAGCAAGTACAGCATGCTTCCCTTATAGGAATTTCCAATAAAGTCCAA	20270
Db	60080	AGAAGACACCCAAAGCAAGTACAGCATGCTTCCCTTATAGGAATTTCCAATAAAGTCCAA	60139
Qy	20271	AGTGCCCTCCACAAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	20330
Db	60140	AGTGCCCTCCACAAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	60199
Qy	20331	TCACATTTGATTAATCTCTTCTGACTAGCATGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTT	20390
Db	60200	TCACATTTGATTAATCTCTTCTGACTAGCATGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTT	60259
Qy	20391	GATTCACAAATCTGTAGTATTTATGATCAATCAATTAATGTCACTAAGAACGTCGACCC	20450
Db	60260	GATTCACAAATCTGTAGTATTTATGATCAATTAATGTCACTAAGAACGTCGACCC	60319
Qy	20451	AGTGTGACTGCTGTAGAACTCCACCTGCTTACATATCAGGAGGATTTGAAATCAGCGGCA	20510
Db	60320	AGTGTGACTGCTGTAGAACTCCACCTGCTTACATATCAGGAGGATTTGAAATCAGCGGCA	60379
Qy	20511	CTCAATTTAGAAATTAAGCTGAAAGGTTGTTCTGACTGGATGCAAAATAAATCTCAAGCGT	20570
Db	60380	CTCAATTTAGAAATTAAGCTGAAAGGTTGTTCTGACTGGATGCAAAATAAATCTCAAGCGT	60439
Qy	20571	GATTGACAGCTTTCTGAGGGGATATTGATTTTCCAGTCAAGAGAGTCAATAGGAGT	20630
Db	60440	GATTGACAGCTTTCTGAGGGGATATTGATTTTCCAGTCAAGAGAGTCAATAGGAGT	60499
Qy	20631	GCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	20690
Db	60500	GCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	60559
Qy	20691	TAGAAGGAGAAATTTAGAGTGAAGTCTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	20750
Db	60560	TAGAAGGAGAAATTTAGAGTGAAGTCTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	60619
Qy	20751	AGAGAGAGGGGCTGCCCTTTCTGTTCTGCTGATCAGTCTCCATAGCTGAACATTCAGAGCA	20810

Db	61700	ACCTGAATGGATTGATAGCAATGATTTGCTCCTAGTGGGAAACAAATGCCAGGATCCTAAA	61750	
Qy	21891	GATTCTAGTTTCTCTAGGACAGATAAAACCAATAATAATTTACATACTTTGGCAAGCAC	21950	
Db	61760	GATTCTAGTTTCTCTAGGACAGATAAAACCAATAATAATTTACATACTTTGGCAAGCAC	61819	
Qy	21951	AACATGGGTGGTGATCAGCTTAAAGATAAAAATTTAAAAATCTATTTAAAGTGAA	22010	
Db	61820	AACATGGGTGGTGATCAGCTTAAAGATAAAAATTTAAAAATCTATTTAAAGTGAA	61879	
Qy	22011	ACATATTTATTTATTTTATACAAGTTACCTGTCTGTTGGAGCAAGAAGT - CAAAAATGTCGCT	22069	
Db	61880	ACATATTTATTTATTTTATACAAGTTACCTGTCTGTTGGAGCAAGAAGTCCAAAAATGTCCT	61939	
Qy	22070	TACTGGGTCAAAAATCAAGATGTTAAAGTAAGTCTGTTTTTGTGAATACAAAAATTCAT	22129	
Db	61940	TACTGGGTCAAAAATCAAGATGTTAAAGTAAGTCTGTTTTTGTGAATACAAAAATTCAT	61999	
Qy	22130	TATGAACAATAATCTCTCCTCATTGTAACATGGGGAAGACGCTTTTGTCTCCACATGC	22189	
Db	62000	TATGAACAATAATCTCTCCTCATTGTAACATGGGGAAGACGCTTTTGTCTCCACATGC	62059	
Qy	22190	ACAATAATTTACTGCTTTTGGTCAACAAGAGGATGTTTCTCTGAGTCAGTCTCTAA	22249	
Db	62060	ACAATAATTTACTGCTTTTGGTCAACAAGAGGATGTTTCTCTGAGTCAGTCTCTAA	62119	
Qy	22250	ACATTAAGTTATCAGTTGGCTTTTCACTGTCTGCGCCATTTCATCAATCTTTATTTCTGATAG	22309	
Db	62120	ACATTAAGTTATCAGTTGGCTTTTCACTGTCTGCGCCATTTCATCAATCTTTATTTCTGATAG	62179	
Qy	22310	TAGAATCACATGCTTTTCTCTTGATCATCCACAGACTGTCAGAGAAATCCAATTAACCT	22369	
Db	62180	TAGAATCACATGCTTTTCTCTTGATCATCCACAGACTGTCAGAGAAATCCAATTAACCT	62239	
Qy	22370	GCTCGATGCTCTTGAACACAGTCAGTAATCTTTTCTCTTTTCTTTTCTTTTCTTTTGA	22429	
Db	62240	GCTCGATGCTCTTGAACACAGTCAGTAATCTTTTCTCTTTTCTTTTCTTTTCTTTTGA	62299	
Qy	22430	GACAGCTCTTGTCTCTCTGCCAGGCTGGAGTGCGATGATTTTCAAGCTCACCATTA	22489	
Db	62300	GACAGCTCTTGTCTCTCTGCCAGGCTGGAGTGCGATGATTTTCAAGCTCACCATTA	62359	
Qy	22490	ACTTCCGCTCTCCAGGTTTAAAGCAATTCCTCCGCTCAGGCTTCTGAGTAGCTGGGACTA	22549	
Db	62360	ACTTCCGCTCTCCAGGTTTAAAGCAATTCCTCCGCTCAGGCTTCTGAGTAGCTGGGACTA	62419	
Qy	22550	CAGGTGTGCCACATGCCAGCTAAATTTTGTATTTTCAATTAAGAGATAGAGTTTTCACCA	22609	
Db	62420	CAGGTGTGCCACATGCCAGCTAAATTTTGTATTTTCAATTAAGAGATAGAGTTTTCACCA	62479	
Qy	22610	TGTTGGCACCAGTAATCATTTTATTTGTATACAGGCTCAGGCTTTATAATGCTAAAGT	22669	
Db	62480	TGTTGGCACCAGTAATCATTTTATTTGTATACAGGCTCAGGCTTTATAATGCTAAAGT	62539	
Qy	22670	TCATTATAAACTCTTAGAGGCGATGCAGCAGCCTACATACTAGTGCATATTTACCAC	22729	
Db	62540	TCATTATAAACTCTTAGAGGCGATGCAGCAGCCTACATACTAGTGCATATTTACCAC	62599	
Qy	22730	ATGCTGATGCGATGTGGAGAAATGAGCACTCAAAGTAGGGCCATGATGTTTTGAAAAACCA	22789	
Db	62600	ATGCTGATGCGATGTGGAGAAATGAGCACTCAAAGTAGGGCCATGATGTTTTGAAAAACCA	62659	
Qy	22790	TGCTCTGTTTCTCTGTTTTTCTCTGGCATCTCAGCTTGCCTATATTTTAAATCT	22849	
Db	62660	TGCTCTGTTTCTCTGTTTTTCTCTGGCATCTCAGCTTGCCTATATTTTAAATCT	62719	
Qy	22850	TCTAGAGCTCAAGTCAAAAAGGCATATTCACCTCTACATCTCCTATGACTCCTTCTCTATGT	22909	
Db	62720	TCTAGAGCTCAAGTCAAAAAGGCATATTCACCTCTACATCTCCTATGACTCCTTCTCTATGT	62779	
Qy	22910	ACTCACACACTTTTTTCTGCCCTCTATATAGCAATTTACTTCATAGACCTTGTTTTGT	22969	
Db	62780	ACTCACACACTTTTTTCTGCCCTCTATATAGCAATTTACTTCATAGACCTTGTTTTGT	62839	

Qy	24050	ATTTTGTGTTAAACAACACGAGGGGCTCTCAGCCCTTCTCAAGGTTTCATAGTTTCACACGAGG	24100
Db	63920	ATTTTGTGTTAAACAACACGAGGGGCTCTCAGCCCTTCTCAAGGTTTCATAGTTTCACACGAGG	63979
Qy	24110	TCCTTCACCTTATGAATATTTACAACCTCACTCGTGAATTTTCAGAAATCCCTCTCTCTATAAAT	24169
Db	63980	TCCTTCACCTTATGAATATTTACAACCTCACTCGTGAATTTTCAGAAATCCCTCTCTCTATAAAT	64039
Qy	24170	CAGCACATAATTTATGAAACCTGTTTTACATTTTCAATCCCAATCGAGAAGTGCAAATAAA	24229
Db	64040	CAGCACATAATTTATGAAACCTGTTTTACATTTTCAATCCCAATCGAGAAGTGCAAATAAA	64099
Qy	24230	TCGTGGAAGACAAATATATTTTATAGTTTTTAATGAGGACATATCAGGATFACHTTAACTTA	24289
Db	64100	TCGTGGAAGACAAATATATTTTATAAGTTTTTAATGAGGACATATCAGGATFACHTTAACTTA	64159
Qy	24290	AAATATGAAGACACCTGAATTTGTGACCTCCACATGTGGGTTTAAACATCTAAAGAATAA	24349
Db	64160	AAATATGAAGACACCTGAATTTGTGACCTCCACATGTGGGTTTAAACATCTAAAGAATAA	64219
Qy	24350	AAACATTTTACCACCTGTTTTTACACAAATTAACCTAAATTCACAGCAAAAGATTTCTTAATC	24409
Db	64220	AAACATTTTACCACCTGTTTTTACACAAATTAACCTAAATTCACAGCAAAAGATTTCTTAATC	64279
Qy	24410	AGACAATTCCTGATTTTCAAGGTTTGAAGACATGTGTGAAGCAACGAGTGAATGCAAACTT	24469
Db	64280	AGACAATTCCTGATTTTCAAGGTTTGAAGACATGTGTGAAGCAACGAGTGAATGCAAACTT	64339
Qy	24470	ACTGACCACTACTATGTATCCAGCACCTTTGTGAGATGCTTTTCACAAAATCAAAATTTCAAT	24529
Db	64340	ACTGACCACTACTATGTATCCAGCACCTTTGTGAGATGCTTTTCACAAAATCAAAATTTCAAT	64399
Qy	24530	TTAATTTCTCACAGCAAAACCCCTCATCTTAGATATTAACAATCCCATTTGGATGGATGTAGAA	24589
Db	64400	TTAATTTCTCACAGCAAAACCCCTCATCTTAGATATTAACAATCCCATTTGGATGGATGTAGAA	64459
Qy	24590	ACTGAGTTGCGAGGAGCTTTAAGTGACTTGCCCTAAAGCCACTGGACGTAAAGTAGATATTCA	24649
Db	64460	ACTGAGTTGCGAGGAGCTTTAAGTGACTTGCCCTAAAGCCACTGGACGTAAAGTAGATATTCA	64519
Qy	24650	GCACATATGTACTGGAATAATCAATGGATGACCTGAATGAATATCTCGAAGGCCACTGAAATTA	24709
Db	64520	GCACATATGTACTGGAATAATCAATGGATGACCTGAATGAATATCTCGAAGGCCACTGAAATTA	64579
Qy	24710	GCCATGAAGACGATAACCCATCATAAAGCCATTTCTCGAACCCCTGGGAATTCATGACCT	24769
Db	64580	GCCATGAAGACGATAACCCATCATAAAGCCATTTCTCGAACCCCTGGGAATTCATGACCT	64639
Qy	24770	GGGGTGATGTATAAGCATATCTATGAATGAAAAATTTTTTAAAAACAAGTTAGGAGA	24829
Db	64640	GGGGTGATGTATAAGCATATCTATGAATGAAAAATTTTTTAAAAACAAGTTAGGAGA	64699
Qy	24830	TGAAGTGCTTAAAAATTTCTTGTTCTCATTTACTAGACTATGAATCCCTGAGCTTTAAACA	24889
Db	64700	TGAAGTGCTTAAAAATTTCTTGTTCTCATTTACTAGACTATGAATCCCTGAGCTTTAAACA	64759
Qy	24890	CCATTGAGTTGCTCAGACGATGAGCTTTGCAGCCACAGGCCAAGTTTCATGCTCATGATT	24949
Db	64760	CCATTGAGTTGCTCAGACGATGAGCTTTGCAGCCACAGGCCAAGTTTCATGCTCATGATT	64819
Qy	24950	CTCTATTTTCTAGCTCTCACAAAACCTTTCTGAAATTTTTTTCTTTTACTATGCAAAATGG	25009
Db	64820	CTCTATTTTCTAGCTCTCACAAAACCTTTCTGAAATTTTTTTCTTTTACTATGCAAAATGG	64879
Qy	25010	GAATCAGATGAGCTCTGCCAAGGAACCTTGTTTAAAGATTAAATGAGTTTTGAGTGTTTGA	25069
Db	64880	GAATCAGATGAGCTCTGCCAAGGAACCTTGTTTAAAGATTAAATGAGTTTTGAGTGTTTGA	64939
Qy	25070	GCACAGCTTAAATCCTCTCTCAGTAGGTATGCCACATTAATTAATGAGTGAGTAAC	25129
Db	64940	GCACAGCTTAAATCCTCTCTCAGTAGGTATGCCACATTAATTAATGAGTGAGTAAC	64999
Qy	25130	ACAGATCAAGAAGGAAAGTTTAAATCAGAAGCACCTTAAACCTAGAAGGAGGTGAGATTTCT	25189

Db	65000	ACAGATCAAGAGGAAGTTTAAATCAGAAGCACCCTAAATCTAGAGGAGCTGAGATCTCT	65059		Db	66080	TGCTTGTGCGCAACAGAGTAAGTGAAGCGAGCTAGACTACTACAAATCATATGAGTCATA	66139	
Qy	25190	GTAATTGGTGATTACTAAGGAATAGAAGGCCATGCCACACCTTGAACCTAAATACAAAAGC	25249		Qy	26270	AACAGTGGCAAAAAGTCTCTAAAAAGAAAAGCTTAGCAGAAAAACATCCAAATAGACAAAAT	26329	
Db	65060	GTAATTGGTGATTACTAAGGAATAGAAGGCCATGCCACACCTTGAACCTAAATACAAAAGC	65119		Db	66140	AACAGTGGCAAAAAGTCTCTAAAAAGAAAAGCTTAGCAGAAAAACATCCAAATAGACAAAAT	66199	
Qy	25250	CAATGATCAGGTGCTTCAAGTTGATTTACATCAGAGCTAACACTATCTCTTTGCAAGTGTA	25309		Qy	26330	AGTGTGAGAAAATTTCTGGATAAATAGTATCAGAAAAGTTTACTGAGAGTAATTTT	26389	
Db	65120	CAATGATCAGGTGCTTCAAGTTGATTTACATCAGAGCTAACACTATCTCTTTGCAAGTGTA	65179		Db	66200	AGTGTGAGAAAATTTCTGGATAAATAGTATCAGAAAAGTTTACTGAGAGTAATTTT	66259	
Qy	25310	TTAGTCCATTCTCATCTAGATTAAGAAAACACCCAGAGCTGGTAGTTTATTAAGAAAA	25369		Qy	26390	GAAAACTTTAATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTGCGCAA	26449	
Db	65180	TTAGTCCATTCTCATCTAGATTAAGAAAACACCCAGAGCTGGTAGTTTATTAAGAAAA	65239		Db	66260	GAAAACTTTAATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTGCGCAA	66319	
Qy	25370	GAGGTTTAATGGCTCACAGTTATGCAATGCCCTGGGAGGCTTAAGGAAACCTTCAATCAT	25429		Qy	26450	TACTATCTGTGAGGCTCTCCAGATTACTGATGCTTATCTTAGAGCCCTTATAGGGAAGACA	26509	
Db	65240	GAGGTTTAATGGCTCACAGTTATGCAATGCCCTGGGAGGCTTAAGGAAACCTTCAATCAT	65299		Db	66320	TACTATCTGTGAGGCTCTCCAGATTACTGATGCTTATCTTAGAGCCCTTATAGGGAAGACA	66379	
Qy	25430	GGCAGAGGCAAGGAGAACCAAGGCACGCTTTACATGCTGGCAGGAGGAGGAGCATGT	25489		Qy	26510	GCAGAGCAATTAATAGAAAATATCTTGGTTCTGTGCAGAGTTTTCGAAGCAATTTCAAATAA	26569	
Db	65300	GGCAGAGGCAAGGAGAACCAAGGCACGCTTTACATGCTGGCAGGAGGAGGAGCATGT	65359		Db	66380	GCAGAGCAATTAATAGAAAATATCTTGGTTCTGTGCAGAGTTTTCGAAGCAATTTCAAATAA	66439	
Qy	25490	GTGCAAGTGTAGGGAACTGCCCTTTATAAATCATCAGATCTGTGCGCACTCACTCACT	25549		Qy	26570	TAACAGTACTATCATTTTATGAGGCTGTAGACTCTTTCATTACCTTAATCCTTAACAC	26629	
Db	65360	GTGCAAGTGTAGGGAACTGCCCTTTATAAATCATCAGATCTGTGCGCACTCACTCACT	65419		Db	66440	TAACAGTACTATCATTTTATGAGGCTGTAGACTCTTTCATTACCTTAATCCTTAACAC	66499	
Qy	25550	ATCACAAGATAGCATGGGAAACCAATCCCATGATTCAAATATCTCCATCTTGTCTCT	25609		Qy	26630	AAATTTGCAAGTGCTTATAATTTAGAGCCATTTTACAAAAGAGAAGAAAATAGAGAAATCAG	26689	
Db	65420	ATCACAAGATAGCATGGGAAACCAATCCCATGATTCAAATATCTCCATCTTGTCTCT	65479		Db	66500	AAATTTGCAAGTGCTTATAATTTAGAGCCATTTTACAAAAGAGAAGAAAATAGAGAAATCAG	66559	
Qy	25610	CCCTTGACATGTGGGATTTATGGGATTTATGGGATTTGCAATTCAGATGAGATTTGGGT	25669		Qy	26690	GGTCTGTGAAGTGACTTCTCCAAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGAAAT	26749	
Db	65480	CCCTTGACATGTGGGATTTATGGGATTTATGGGATTTGCAATTCAGATGAGATTTGGGT	65539		Db	66560	GGTCTGTGAAGTGACTTCTCCAAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGAAAT	66619	
Qy	25670	GGGACACATGATCACTATATAGCAAGTAAAGACACTCAGTGAGTTGGATCTCTCAG	25729		Qy	26750	TTATTTACAGTTTGTGACTCTCAAGTCCATGCTCTTTCCATTCGAAAGTCTCTTCTTC	26809	
Db	65540	GGGACACATGATCACTATATAGCAAGTAAAGACACTCAGTGAGTTGGATCTCTCAG	65599		Db	66620	TTATTTACAGTTTGTGACTCTCAAGTCCATGCTCTTTCCATTCGAAAGTCTCTTCTTC	66679	
Qy	25730	CACCAGGAGGCTTACAAGCATATATGCTCTAGGAGCAGTGTAGTCTCTTAAAGTCTA	25789		Qy	26810	TTTTGCTCTATTCTATTAAATTTATGCCAAACAATTTTAAATTTTAAATTTTAAATTTT	26869	
Db	65600	CACCAGGAGGCTTACAAGCATATATGCTCTAGGAGCAGTGTAGTCTCTTAAAGTCTA	65659		Db	66680	TTTTGCTCTATTCTATTAAATTTATGCCAAACAATTTTAAATTTTAAATTTTAAATTTT	66739	
Qy	25790	GTGGGGATTAAGGAAACCAATCCCATATAATTTTCCAATGCTTACAGAAAATAA	25849		Qy	26870	CACCTTGGTAAAGGTACCAATATACACATGTTCCAGGAACTCAATTAAGCTTAACCATC	26929	
Db	65660	GTGGGGATTAAGGAAACCAATCCCATATAATTTTCCAATGCTTACAGAAAATAA	65719		Db	66740	CACCTTGGTAAAGGTACCAATATACACATGTTCCAGGAACTCAATTAAGCTTAACCATC	66799	
Qy	25850	GCACAGCAACACAGGAACACACATTTCTTTTACAGAGTAATTCAGTGGGAAAATG	25909		Qy	26930	TTTCAATATAGAACTATTATTAAATTAATGTTATATTAATTAAGCAACACAAAGTTAT	26989	
Db	65720	GCACAGCAACACAGGAACACACATTTCTTTTAAAGAGTAATTTGAGTGGAAAATG	65779		Db	66800	TTTTCAATAAGAACTATTATTAAATTAATGTTATATTAATTAAGCAACACAAAGTTAT	66859	
Qy	25910	CACATTTGTTCAATCCGACGCTAAAAGTTTACCTATGCTTTCCACTGTCAACTGGATTTT	25969		Qy	26990	ATTAATGCTCTATTACTACTGATGTCAACAGTACCTCTCTTAAATTTTACAGAGATGTAGTTA	27049	
Db	65780	CACATTTGTTCAATCCGACGCTAAAAGTTTACCTATGCTTTCCACTGTCAACTGGATTTT	65839		Db	66860	ATTAATGCTCTATTACTACTGATGTCAACAGTACCTCTCTTAAATTTTACAGAGATGTAGTTA	66919	
Qy	25970	CTTATTGATTGCAATTTGAATGACATGCCCTAGATGAGGGGAATTAACCTTTGATAATGAGG	26029		Qy	27050	CAGATATCTGAAGACTGACTGATCTGACTCATCTGCTGCTGGTGGCGCAACAGCTTTTGGA	27109	
Db	65840	CCTATTGATTGCAATTTGAATGACATGCCCTAGATGAGGGGAATTAACCTTTGATAATGAGG	65899		Db	66920	CAGATATCTGAAGACTGACTGATCTGACTCATCTGCTGCTGGTGGCGCAACAGCTTTTGGA	66979	
Qy	26030	TGGGGTTAGGATATCCACAAGACGACCAACTCGCTCTAGGATGAAGAGAGGTTGGCAC	26089		Qy	27110	AAATTTCTTAAACCAAGTATCAAAATAGCAGACAGAAAATTTGCAAGCACTCAGTTTCTAA	27169	
Db	65900	TGGGGTTAGGATATCCACAAGACGACCAACTCGCTCTAGGATGAAGAGAGGTTGGCAC	65959		Db	66980	AAATTTCTTAAACCAAGTATCAAAATAGCAGACAGAAAATTTGCAAGCACTCAGTTTCTAA	67039	
Qy	26090	AGGCACAGGAGGAAAAACAACTGAAAGTTGTCCCACTGCTGAGATTTTCTTAAATATT	26149		Qy	27170	AAATTTCTTAAACCAAGTATCAAAATAGCAGACAGAAAATTTGCAAGCACTCAGTTTCTAA	27229	
Db	65960	AGGCACAGGAGGAAAAACAACTGAAAGTTGTCCCACTGCTGAGATTTTCTTAAATATT	66019		Db	67040	AAATTTCTTAAACCAAGTATCAAAATAGCAGACAGAAAATTTGCAAGCACTCAGTTTCTAA	67099	
Qy	26150	TCATGTGTGGCCCTCATAGACACACAAATATGATTAACAAACAATATGTTTATGAA	26209		Qy	27230	AAATTTCTTAAACCAAGTATCAAAATAGCAGACAGAAAATTTGCAAGCACTCAGTTTCTAA	27289	
Db	66020	TCATGTGTGGCCCTCATAGACACACAAATATGATTAACAAACAATATGTTTATGAA	66079		Db	67100	AAATTTCTTAAACCAAGTATCAAAATAGCAGACAGAAAATTTGCAAGCACTCAGTTTCTAA	67159	
Qy	26210	TGCTTCTCGCAACAGCTAAGTGGGAGGAGTACTTCAATCATATGAGTCATA	26269		Qy	27290	TCATTTAAATTTTAAAGAACTTCTTCTGACTTAAAGAACTCAGAGAAATGAAACA	27349	
				Db	67160	TGATTTAAATTTTAAAGAACTTCTTCTGACTTAAAGAACTCAGAGAAATGAAACA	67219		

QY	27350	TACTGATATATAAACATTTATTTTCAATTTATTTCTCAGTTCCTTAAGCTAGTTATTTACCTG	27409
DB	67220	TACTGATATATAAACATTTATTTTCAATTTATTTCTCAGTTCCTTAAGCTAGTTATTTACCTG	67279
QY	27410	TAAATATTTTGCATAATTTAGAGTCAAAATGTTTTAGATTTTAGAGGAAATGCTCATGAGAA	27469
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SEQUENCE, 18 unordered pieces.
ACCESSION AC067870
VERSION AC067870.3 GI:8671974
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 160345)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-475J2
Unpublished
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bedalov,F.,
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Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 23, 2000 this sequence version replaced gi:8099852.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIGR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8810
Center clone name: 475_J_2
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 151812 bases at least Q40
Consensus quality: 156075 bases at least Q30
Consensus quality: 157717 bases at least Q20
Insert size: 163000; agarose-fp
Library size: 158645; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Db	78955	TTTACAGAGAAAGCAATGCTGACAGATTTTGTACACACAGCGCTTGCCTTTACAAGAGCT	78896
Qy	3296	CCTGAGGAGCACCACATGGAAGAAAGCAACTGGTACAGCCACTGCAGGCAAAACATCCC	3355
Db	78895	CCTGAGGAGCACCACATGGAAGAAAGCAACTGGTACAGCCACTGCAGGCAAAACATCCC	78836
Qy	3356	AAATTTGAAGACCATTTGCTTATGAAGAAAGTGCATCAACTTAACGGGCAAAATAACCA	3415
Db	78835	AAATTTGAAGACCATTTGCTTATGAAGAAAGTGCATCAACTTAACGGGCAAAATAACCA	78776
Qy	3416	GCTAGTGTCAATATGCGCAGGATCAAAATTCACACATTAATTAATTAACCTTTAAATGTAAT	3475
Db	78775	GCTAGTGTCAATATGCGCAGGATCAAAATTCACACATTAATTAATTAACCTTTAAATGTAAT	78716
Qy	3476	GGCTAAATTTCCCAATTAAGAGACACAGACTGGCAAAATTTGGATAAAGAGTCAAGACCA	3535
Db	78715	GGCTAAATTTCCCAATTAAGAGACACAGACTGGCAAAATTTGGATAAAGAGTCAAGACCA	78656
Qy	3536	TCAGTGTGCTGATTTCAGGAGGCCATCTCACATGAAAAGACACACATAGGCTCAAAATA	3595
Db	78655	TCAGTGTGCTGATTTCAGGAGGCCATCTCACATGAAAAGACACACATAGGCTCAAAATA	78596
Qy	3596	AAGGATGGAAGAAATTTACCAAGTAAATGGAATAACAAAAAAGAGAGAGGTTGCA	3655
Db	78595	AAGGATGGAAGAAATTTACCAAGTAAATGGAATAACAAAAAAGAGAGAGGTTGCA	78536
Qy	3656	ATCCTAGTCTCTGATTAACCAACAGACTTTAAACCAACAAAGATCAAAAGAGAGAGG	3715
Db	78535	ATCCTAGTCTCTGATTAACCAACAGACTTTAAACCAACAAAGATCAAAAGAGAGAGG	78476

QY	3716	CATTACATAATGGTAAAGGCATCAATGGAACAAGAGAGCTAACTATCCTAAATATACAT	3775	4796	ATCAGAGAAATAAAGACAAAGACAAAGACAAAGATATGTTTGAAGTAGGGTCAGGGGCAAC	4855
Db	78475	CATTACATAATGGTAAAGGCATCAATGGAACAAGAGAGCTAACTATCCTAAATATACAT	78416	77395	ATCAGAGAAATAAAGACAAAGACAAAGACAAAGATATGTTTGAAGTAGGGTCAGGGGCAAC	77336
QY	3776	GCACCCCAATACAGAGACACCCAGATTCATTAAGCAAGTCTTAGAGACCTACAAAGAGAC	3835	4856	TTGCCCTCTAATGACARAGGCCCTGAGCTTTACACACCCCTCTGTATTTATTAGGCAAAA	4915
Db	78415	GCACCCCAATACAGAGACACCCAGATTCATTAAGCAAGTCTTAGAGACCTACAAAGAGAC	78356	77335	TTGCCCTCTAATGACARAGGCCCTGAGCTTTACACACCCCTCTGTATTTATTAGGCAAAA	77276
QY	3836	TTTGACTCCACACAATAAATAGTGGGAGTCTAAATAATAATAATAGACACTTTAAACACCCA	3895	4916	GAGATAGCAGAGAGGTGAGTTGGAAGAAGAGGTGAGCTGTTAGGTCAGAGTAGGCTGTC	4975
Db	78355	TTTGACTCCACACAATAAATAGTGGGAGTCTAAATAATAATAATAGACACTTTAAACACCCA	78296	77275	GAGATAGCAGAGAGGTGAGTTGGAAGAAGAGGTGAGCTGTTAGGTCAGAGTAGGCTGTC	77216
QY	3896	CTGCCAATATTAGGCGAGATCAATGAGACAGAGAAATTAACAAGGATATCCAGGAGTTGAAC	3955	4976	AAGACTGCATTCTCTCAACAATAGGCTCTAGATGTCCAGTAGATAACCTCAAGAGGCCA	5035
Db	78295	CTGCCAATATTAGGCGAGATCAATGAGACAGAGAAATTAACAAGGATATCCAGGAGTTGAAC	78236	77215	AAGACTGCATTCTCTCAACAATAGGCTCTAGATGTCCAGTAGATAACCTCAAGAGGCCA	77156
QY	3956	TGAGCTCTGGACCAAGGGGACCTAATAGATATCTACAGAACTCCCCACCCCAATCAACA	4015	5036	GTGCCAGGAGTAGTGCCCTCAGCAAAACCTTTAGGGCAGGCACAGAAAGTAAAGTTTGCC	5095
Db	78235	TGAGCTCTGGACCAAGGGGACCTAATAGATATCTACAGAACTCCCCACCCCAATCAACA	78176	77155	GTGCCAGGAGTAGTGCCCTCAGCAAAACCTTTAGGGCAGGCACAGAAAGTAAAGTTTGCC	77096
QY	4016	GAATATACACTCTCTCAGCATCACATTACACCTATTTTAAATTTGACCATGTAATTTTA	4075	5096	CACATTCGTATTACAGATAAACAAGTTTGTGTTTGTATCAAGTAGCCTCCAGTGGAAATGC	5155
Db	78175	GAATATACACTCTCTCAGCATCACATTACACCTATTTTAAATTTGACCATGTAATTTTA	78116	77095	CACATTCGTATTACAGATAAACAAGTTTGTGTTTGTATCAAGTAGCCTCCAGTGGAAATGC	77036
QY	4076	AGTAAACACTCTCTCAGCAATGCAAAAGAACAGAAATCCTAACAACACAGTCTCTCAGAC	4135	5156	TGAGTTGTCATGATCCTTTGGCTTTTGGCTCCCAAAACACATACACCTCTCAAGA	5215
Db	78115	AGTAAACACTCTCTCAGCAATGCAAAAGAACAGAAATCCTAACAACACAGTCTCTCAGAC	78056	77035	TGAGTTGTCATGATCCTTTGGCTTTTGGCTCCCAAAACACATACACCTCTCAAGA	76976
QY	4136	TACAGTGCATCTATTAGAACCTCAGAAATTAAGAAACTACTCAAAATCAACAACATPACA	4195	5216	CTAAACAGGAAGAAGTCAAAATCCTCGAATATATACCAAGTAACAAGTCTTAAATTTGAAGCA	5275
Db	78055	TACAGTGCATCTATTAGAACCTCAGAAATTAAGAAACTACTCAAAATCAACAACATPACA	77996	76975	CTAAACAGGAAGAAGTCAAAATCCTCGAATATATACCAAGTAACAAGTCTTAAATTTGAAGCA	76916
QY	4196	TGAAACTGAAACACCTGCTCCTGAATGACTACTGGTGAATTAACAAATCAAGGCAAAA	4255	5276	GTAAATTCATAGCTTACCACCAACCAAAAGTCCAGGACACAGGATTTACAGCCAAATTC	5335
Db	77995	TGAAACTGAAACACCTGCTCCTGAATGACTACTGGTGAATTAACAAATCAAGGCAAAA	77936	76915	GTAAATTCATAGCTTACCACCAACCAAAAGTCCAGGACACAGGATTTACAGCCAAATTC	76856
QY	4256	ATAAAGATGTTCTTTGAAACCAATGAGAACAAGACACAATGTACCAGAAATCTCTGGGGC	4315	5336	TACCAGAGGTACAAAGAGAAGCTGGTACTATTCCTCTGAAACTATTTCCAAAAATAGAA	5395
Db	77935	ATAAAGATGTTCTTTGAAACCAATGAGAACAAGACACAATGTACCAGAAATCTCTGGGGC	77876	76855	TACCAGAGGTACAAAGAGAAGCTGGTACTATTCCTCTGAAACTATTTCCAAAAATAGAA	76796
QY	4316	ATATTTAAAGCAGTGTAGAGGAAATTTATAGCACTAGATGCTTCAAGAGAAACGAG	4375	5396	ATGCGGAATCCTCCCTAACTCATTTTACGAGGCCAGCATCATCTCTGATACCAAACTAG	5455
Db	77875	ATATTTAAAGCAGTGTAGAGGAAATTTATAGCACTAGATGCTTCAAGAGAAACGAG	77816	76795	ATGCGGAATCCTCCCTAACTCATTTTACGAGGCCAGCATCATCTCTGATACCAAACTAG	76736
QY	4376	GAAATATCTAAATAGACACCTTAACATCAATTAAGAACTAGAGAGAGAGAGCAAA	4435	5456	CAGTGACACAAACAAAAAGAGAAATTTACAGCCCATATTCCTGTATGAACATTTGATGTGAA	5515
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QY	4436	ACAAATTCAAAAGCTAGCAGAAGACAAAGAAATTAAGATCAGAGCAGAACTCAAGGAG	4495	5516	AAATCCTCAATTAATAATCTGGCAACCAAAATCCAGCAGCATCAAAAAGCTTATCTACCA	5575
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QY	4496	ATAGAGACACAAAAGCCCTTCAATTAATCAATGAATCCAGAGCTGGTTTTTGAATAA	4555	5576	TGATCAAGTTGGCGTCATCCTCGGATGCAAGGCTGGTTCAAATATATGCAAAATCAATAA	5635
Db	77695	ATAGAGACACAAAAGCCCTTCAATTAATCAATGAATCCAGAGCTGGTTTTTGAATAA	77636	76615	TGATCAAGTTGGCGTCATCCTCGGATGCAAGGCTGGTTCAAATATATGCAAAATCAATAA	76556
QY	4556	GATCAGCAAAATAGACCACTAGACAGACTAATAAAGAGAAAGAGAGAGAGATCAAGA	4615	5636	TGTAGGCCATCACATAAACAAGAACCAATGACAAAAACCATGATTTCTCAATAGATGC	5695
Db	77635	GATCAGCAAAATAGACCACTAGACAGACTAATAAAGAGAAAGAGAGAGAGATCAAGA	77576	76555	TGTAGGCCATCACATAAACAAGAACCAATGACAAAAACCATGATTTCTCAATAGATGC	76496
QY	4616	GATGCAATAAAAATGATAAGGGGATATCACCACCGATCCACAGAAATACAACTATT	4675	5696	AGAAAAGCCCTTTGTCAAAAATTCAAACGCCCTTCATGCTTAAAAATTTCTCAGTAACTAGG	5755
Db	77575	GATGCAATAAAAATGATAAGGGGATATCACCACCGATCCACAGAAATACAACTATT	77516	76495	AGAAAAGCCCTTTGTCAAAAATTCAAACGCCCTTCATGCTTAAAAATTTCTCAGTAACTAGG	76436
QY	4676	ATCAGAGAAATTAATAAACCTCTATGCAAAATAAAGTAACTAGAAATCTAGAGAAATGGAT	4735	5756	TATCGATGGAATGTATCTCAAAAATTAAGAGCTATTTATACAAACCCACAGCAATATC	5815
Db	77515	ATCAGAGAAATTAATAAACCTCTATGCAAAATAAAGTAACTAGAAATCTAGAGAAATGGAT	77456	76435	TATCGATGGAATGTATCTCAAAAATTAAGAGCTATTTATACAAACCCACAGCAATATC	76376
QY	4736	AAATCTCTGACACATATGAGCTCTATGGACTTGGGGGACAGAAACAAAGGGGTGA	4795	5816	ATACTGAATGGCAAAACCTGGAGCATTCCTTTTGAGAACTGGCAACACAGGATGC	5875
Db	77455	AAATCTCTGACACATATGAGCTCTATGGACTTGGGGGACAGAAACAAAGGGGTGA	77396	76375	ATACTGAATGGCAAAACCTGGAGCATTCCTTTTGAGAACTGGCAACACAGGATGC	76316
				5876	CCTCTCTCACCACCTCTATTCAAGATACTATTGGAAGTTCTTGCCAGGGCAATCAGGCAA	5935

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Db	35964	GGACTGATATCAAGTCCCAAGACATAGTACTCAGTTTAAAAAGACATAAATGGCAACAGC	36023	Db	37044	CCATGAGGCTTCACTTAAAGTGGAGAAAGGACAGAGGACGACAGACATCCACAAGTTCT	37103
QY	10961	TCAACAGTGTATATTAAGAAGTTAAGCTTGAAGGTGACAAAAAGCTGGTTATAGTGGG	11020	QY	12041	AGCTATGAGGTTTCCAAAAATAACAGAAAAAGAGATTTCTTGACTTTATATATGTTA	12100
Db	36024	TCAACAGTGTATATTAAGAAGTTAAGCTTGAAGGTGACAAAAAGCTGGTTATAGTGGG	36083	Db	37104	AGCTATGAGGTTTCCAAAAATAACAGAAAAAGAGATTTCTTGACTTTATATATGTTA	37163
QY	11021	AGTTTATAACATGCTCATGAATTTTGAANAATGCAATCATGATATCTGTCATATTTACTT	11080	QY	12101	GGTATAATCATGACCCAAAACACTCCCTCTATTTGCTAGAGAGGAAAACCTCCTTCGGGG	12160
Db	36084	AGTTTATAACATGCTCATGAATTTTGAANAATGCAATCATGATATCTGTCATATTTACTT	36143	Db	37164	GGTATAATCATGACCCAAAACACTCCCTCTATTTGCTAGAGAGGAAAACCTCCTTCGGGG	37223
QY	11081	CAATAGATGCGTCTGCTGAGACTCTAGGTTACTATGAGGTACTCTAGTTGCAAGTTT	11140	QY	12161	AAATTTATTTTCTGTTTCTTCTCAATTTGAAATTTAGTACTTTTTTTTCAATAA	12220
Db	36144	CAATAGATGCGTCTGCTGAGACTCTAGGTTACTATGAGGTACTCTAGTTGCAAGTTT	36203	Db	37224	AAATTTATTTTCTGTTTCTTCTCAATTTGAAATTTAGTACTTTTTTTTCAATAA	37283
QY	11141	AACCTTACAGAACTAAATAGTTAAATGATTTTACAGACCTTTAGAGGATTTATGACTAC	11200	QY	12221	CAGAGCTTCAACATGTAACCAACAAAGTACTATTTCTTTTACCTCAAACTCTGAAGGTCAA	12280
Db	36204	AACCTTACAGAACTAAATAGTTAAATGATTTTACAGACCTTTAGAGGATTTATGACTAC	36263	Db	37284	CAACGCTTCAACATGTAACCAACAAAGTACTATTTCTTTTACCTCAAACTCTGAAGGTCAA	37343
QY	11201	ATGTTTACAGCTACCAATTCGAGAAACATAATGGAAGGCTGGTGGGCACTACATTTCA	11260	QY	12281	CAGTGTATTTACTCTAACCTCATATTTTCATGTATATAATACAGATGCTCGTTGACTTATGAT	12340
Db	36264	ATGTTTACAGCTACCAATTCGAGAAACATAATGGAAGGCTGGTGGGCACTACATTTCA	36323	Db	37344	CAGTGTATTTACTCTAACCTCATATTTTCATGTATATAATACAGATGCTCGTTGACTTATGAT	37403
QY	11261	GAGCATGGCATTAGCATTTGGGTATCACTCATGACACAGATGGGCTTGTCTGCTGGGA	11320	QY	12341	GGGGCTATATCTCTGATAAACCCATTTGGAGGTTTAAAAATATTTTAACTTGAAATGCAATTA	12400
Db	36324	GAGCATGGCATTAGCATTTGGGTATCACTCATGACACAGATGGGCTTGTCTGCTGGGA	36383	Db	37404	GGGGCTATATCTCTGATAAACCCATTTGGAGGTTTAAAAATATTTTAACTTGAAATGCAATTA	37463
QY	11321	GTACCTTGGCCCATGTGGCAAGTTTGGCCCTTTGGCAGGAAGCCCTGATGTGAAGTAGA	11380	QY	12401	ATACCCCCCATTAACCCCACTGAAAGTAAAAAAGTAAAAAATCTAAATCTAACCATCAT	12460
Db	36384	GTACCTTGGCCCATGTGGCAAGTTTGGCCCTTTGGCAGGAAGCCCTGATGTGAAGTAGA	36443	Db	37464	ATACCCCCCATTAACCCCACTGAAAGTAAAAAAGTAAAAAATCTAAATCTAACCATCAT	37522
QY	11381	TTGAGAAGGAGAGAGTGTGCAAGTTTGTATTAATCTTAAACAAGAGTTCACTAACCTGTAA	11440	QY	12461	TCAGGATATCTGTTACCAATTTATTTAAATACATCTCTTAACCTGATGATAAATG	12520
Db	36444	TTGAGAAGGAGAGAGTGTGCAAGTTTGTATTAATCTTAAACAAGAGTTCACTAACCTGTAA	36503	Db	37523	TCAGGATATCTGTTACCAATTTATTTAAATACATCTCTTAACCTGATGATAAATG	37582
QY	11441	GTGAGTCATCAGGGAAGAAATGTAATCAGAACTGAGAAAGCCAGACCGCTCTCATCTA	11500	QY	12521	CAAAATTTTAAATACAAAATTTTACCTTAGAACAAAGAAAGTCAATTTTTTTTTCATTTTG	12580
Db	36504	GTGAGTCATCAGGGAAGAAATGTAATCAGAACTGAGAAAGCCAGACCGCTCTCATCTA	36563	Db	37583	CAAAATTTTAAATACAAAATTTTACCTTAGAACAAAGAAAGTCAATTTTTTTTTCATTTTG	37642
QY	11501	ATTCCACCACATCTGCTGTACTTTATAGTCTTCAAGATGCTTCAATTCACCCAGTATC	11560	QY	12581	TCATAGATGCTTAAAGTATTTAGATGCTATAAATGTGCCAAGTACAGATAGGTATAGG	12640
Db	36564	ATTCCACCACATCTGCTGTACTTTATAGTCTTCAAGATGCTTCAATTCACCCAGTATC	36623	Db	37643	TCATAGATGCTTAAAGTATTTAGATGCTATAAATGTGCCAAGTACAGATAGGTATAGG	37702
QY	11561	CCCAGTGTGAAGACACATGTGTATCATTTGCCATTTGCAAGATGATGAATTAACCTT	11620	QY	12641	CTTGTGCCATTTCAACAAGTACTCAGGCTTGTGTGTAATTTAAATTTCAATTTAGTTA	12700
Db	36624	CCCAGTGTGAAGACACATGTGTATCATTTGCCATTTGCAAGATGATGAATTAACCTT	36683	Db	37703	CTTGTGCCATTTCAACAAGTACTCAGGCTTGTGTGTAATTTAAATTTCAATTTAGTTA	37762
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QY	11681	TACCTAGCATTTCAACCACCAATTTGTTTTTATTCCTTACAAATTTTCAATTAAGATTTTG	11740	QY	12761	CAGCCACATGTTGCTAGTGACTACCATATFGGAACATFGCAATATAGGTTATTCCTATCA	12820
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QY	11801	AACTCAAAATTTAGTGTATTTATGGGATTTAAGTGAAGAAACCTGAGGCCCTGGGAAGTT	11860	QY	12881	AGAGCAAGAACAGAGAAAATTAACATCTATCTTTTATCTTTTGTGCTCTTCTTATGTTTTT	12940
Db	36864	AACTCAAAATTTAGTGTATTTATGGGATTTAAGTGAAGAAACCTGAGGCCCTGGGAAGTT	36923	Db	37943	AGAGCAAGAACAGAGAAAATTAACATCTATCTTTTATCTTTTGTGCTCTTCTTATGTTTTT	38002
QY	11861	TTAAGTGGCTGTCTCAGTTGCCCTCCATGTGCCAAGCTGGAACCAAGAACCCACATC	11920	QY	12941	GGCTGTTGACTAAATGGATACAGCCAGGCCACCAATCATGAAAACAGTTCAGTAATAA	13000
Db	36924	TTAAGTGGCTGTCTCAGTTGCCCTCCATGTGCCAAGCTGGAACCAAGAACCCACATC	36983	Db	38003	GGCTGTTGACTAAATGGATACAGCCAGGCCACCAATCATGAAAACAGTTCAGTAATAA	38062
QY	11921	TTTTCTAGTCTGCAAGTTTCTGCTCTATTCCTCTATTCCTCTCTTGGTAGGAAAACATCACA	11980	QY	13001	TTTTTATAGTCTACTACTTTTAGAAAATATCTCTCTCTCTTCAATATACATATCAAGAG	13060
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QY	11981	CCATGAGGCTTCACTTAAAGTGGAGAAAGGACAGAGGACAGAGACTTCCACAAGTTCT	12040	QY	13061	AAGAGAACTGAAATTAATAGTTTCTTCTAAATGCTTACACAATACCTTTTCTTGGAACTCT	13120
				Db	38123	AAGAGAACTGAAATTAATAGTTTCTTCTAAATGCTTCTACACAATACCTTTTCTTGGAACTCT	38182

Qy	13121	CCCTTTAACAAAAAATCACTACCCAAATATCTTTTATATCTATGATGGGTTTCAGGACA	13180
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Qy	13181	CTGTACTCCCAATGTTTAACTCAAGGAATTTGAGAAAACAGAAAAGCAGAAAATC	13240
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Db	38363	CCTTCCCATGTAGCAAGTCATAAAGACCTCATGCGAGAGGTGCCCTGTTATATCCAGAA	38422
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Db	39023	TTTGTGTTATAGTGCCTCAGCCATGAACCTTAGGAAGGGTGGAGAAAGGATTTTTCCTA	39082
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DB	39443	GAAACTGGTTTCCATTTCTCAGAGGTAGAAATACAGACACAGAAATTCAGAAATAAAGGAC	39502
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RESULT 6
LOCUS AX164746/c 1587 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3 from Patent WO0125437.
ACCESSION AX164746
VERSION AX164746.1 GI:14545599
KEYWORDS human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1587)
Shinkets,R.A., Lichenstein,H., Herrmann,J.L., Boldog,F.L.,
Minskoff,S. and Jeffers,M.
Growth factor polypeptides and nucleic acids encoding same
Patent: WO 0125437-A 3 12-APR-2001;
Curagen Corporation (US)
FEATURES
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BASE COUNT 522 a 298 c 329 g 438 t
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DEFINITION Sequence 18 from Patent WO0125437.
ACCESSION AX164761
VERSION AX164761.1 GI:14545604
KEYWORDS human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1734)
Shinkets,R.A., Lichenstein,H., Herrmann,J.L., Boldog,F.L.,
Minskoff,S. and Jeffers,M.
Growth factor polypeptides and nucleic acids encoding same
Patent: WO 0125437-A 18 12-APR-2001;
Curagen Corporation (US)
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BASE COUNT 530 a 365 c 382 g 457 t
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ACCESSION	AXI64744
VERSION	AXI64744.1 GI:14545598
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SOURCE	human.
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1828)
AUTHORS	Shimkets,R.A., Lichenstein,H., Herrmann,J.L., Boldog,F.L., Minskoff,S. and Jeffers,M.
TITLE	Growth factor polypeptides and nucleic acids encoding same
JOURNAL	Patent: WO 0125437-A 1 12-APR-2001;
FEATURES	Curagen Corporation (US)
source	Location/Qualifiers l..1828
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Best Local Similarity	100.0%; Pred. No. 2.2e-310;
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 AF335584 1828 bp mRNA linear PRI 24-APR-2001
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 DEFINITION
 ACCESSION AF335584
 VERSION AF335584.1 GI:13744335
 KEYWORDS
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1828)
 AUTHORS LaRochele W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
 Giese M.A., Wolke N.A., Sullivan C., Beilodog F.B., Yang M.,
 Vernet C., Burgess C.E., Fernandez E., Deegler L.L., Rittman B.,
 Shimkets J., Shinkets R., Rothberg J., May and Lichenstein, H.S.
 PDGF-D, a new protease, activated growth factor
 JOURNAL Biol. Cell Biol. 3 (5) 517-521 (2001)
 MEDLINE 21231380
 PUBMED 11311882
 REFERENCE 2 (bases 1 to 1828)
 AUTHORS LaRochele W.J., Jeffers M., Yang M., Vernet C., Burgess C.E.,
 Fernandez E., Shinkets R.A. and Lichenstein, H.S.
 Direct Submission
 TITLE Submitted (11-JAN-2001) Development, CuraGen Corporation, 322 East
 JOURNAL Main Street, Branford, CT 06403, USA
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 /organism="Homo sapiens"
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BASE COUNT 572 a 380 c 385 g 491 t
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Best Local Similarity 100.0%; Pred. No. 2.2e-310;
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QY 61 GCAAGATTCAAAATGTTTGTGCTTTCAAAATTTAAATAATATATATACCAAGATGCTTTCTTTAGAGA 120
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DB 1698 CTAAAGACATGTTTCATATATTTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 1639
QY 181 AACTCAACATATGTAGCTCTCGTGACCTGCTTATATATACCAAAAAAATTTTAT 240
DB 1638 AACTCAACATATGTAGCTCTCGTGACCTGCTTATATATACCAAAAAAATTTTAT 1579
QY 241 CTATATACACATAGACATGAATATATTTCTGTGTGTTTGCATATATATAAAGTCT 300
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DB 1518 ACTATATTAATGCAATCCTATATTTCTGTGTGTTTGCATATATATAAAGTCT 1459
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QY 421 CAGGCTAGTAGTAAGTTTGTGCTGTAGGAAAGGCTCTTATCTACCCCTCCTTAA 480
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RESULT 10
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LOCUS
DEFINITION Sequence 3 from Patent WO0189450.
ACCESSION AX365307
VERSION AX365307.1 GI:18697038
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Beals, J.M., Gonzalez-Dewhitt, P.A., Hammond, L.J., Lu, J., Na, S.,
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Su, E.W., Switzer, D.R. and Wroblewski, V.J.
Treating musculoskeletal disorders using lp85 and analogs thereof
Patent WO 0189450-A.3 29-NOV-2001;
ELI LILLY AND COMPANY (US)
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Best Local Similarity 100.0%; Pred. No. 2e-310;
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QY 1 GTATATCTAAGAAAGCCTCATCTTTTGCTTTCAAAATTTAAATAATATATACCAAGATGCTTTCTTTAGAGA 60
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QY 61 GCAAGATTCAAAATGTTTGTGCTTTCAAAATTTAAATAATATATATACCAAGATGCTTTCTTTAGAGA 120
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DB 1432 ACTATATTAATGCAATCCTATATTTCTGTGTGTTTGCATATATATAAAGTCT 1373
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ORIGIN

Query Match	2.2%	Score 652;	DB 9;	Length 4070;
Best Local Similarity	100.0%;	Pred. No. 2e-310;		
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Db	2016	GCAAGATTCAAAATGTTTTGTTGTTCAAAATTTAAAAATTAATATATCTCCATAAATTTT	1957	
Qy	121	CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT	180	
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Qy	421	CAGGCTAGTAGTAAGTTTGTTGCTGGTAGCAAAAGGGTCTCTTATCTCAACCTCCCTAA	480	
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LOCUS				
DEFINITION				
ACCESSION	AF336376			
VERSION	AF336376.1			
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REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBLISHED				
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JOURNAL				
MEDLINE				
PUBLISHED				

TITLE	source
JOURNAL	Alitalo,K. and Eriksson,U. Direct Submission Submitted (15-JAN-2001) Ludwig Institute for Cancer Research, Nobelstsvag 3 (Box 240), Stockholm S-171 77, Sweden
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BASE COUNT	701 a 464 c 490 g 598 t

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QY	61	GCAAGATTCAAAATTTGTTTGCTTTCAAAATTTAAAAATTAATATCTCCTAAATTTT	120				
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DB	1692	CTAAAGACATGTTTCATATATTTGACCATCCCTTATTTGGCAAGAGATTTTAAAGAGTCT	1633				
QY	181	AACTCAAAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACAATTTGAT	240				
DB	1632	AACTCAAAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACAATTTGAT	1573				
QY	241	CTATATACACATAGACATGAATATATTTCTGCTGTGCTTTGTGCGATATATAACCTCAAC	300				
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DB	1512	ACTATTATTAATGCAATCCTATATCTTACGTTAGGTTAGAACTTGATGATACCTTCTAC	1453				
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RESULT 14
AY027518/c 3710 bp mRNA linear PRI 17-JUL-2002
LOCUS
DEFINITION Homo sapiens iris-expressed growth factor short form (IEGF) mRNA,
complete cds, alternatively spliced.
ACCESSION AY027518
VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 3710)
AUTHORS Wistow,G., Berstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed-sequence tag analysis of adult human iris for the NEIBank
Project: steroid response factors and similarities with retinal
pigment epithelium
JOURNAL Mol. Vis. 8, 185-195. (2002)
MEDLINE 22103462
PUBMED 12107412

REFERENCE 2 (bases 1 to 3710)
AUTHORS Wistow,G.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD
20892-2740, USA

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BASE COUNT 1169 a 724 c 703 g 1114 t
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QY 601 GTCCTAGCTCTACCCCTCTCTTGTGATGTGGCAGGCTCAAACTGTAATACCT 652
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Db 1111 GTCCTAGCTCTACCCCTCTCTTGTGATGTGGCAGGCTCAAACTGTAATACCT 1060
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RESULT 15
AY027517/c 3729 bp mRNA linear PRI 17-JUL-2002
LOCUS
DEFINITION Homo sapiens iris-expressed growth factor long form (IEGF) mRNA,
complete cds, alternatively spliced.
ACCESSION AY027517
VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3729)
AUTHORS Wistow,G., Berstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed-sequence tag analysis of adult human iris for the NEIBank
Project: steroid response factors and similarities with retinal
pigment epithelium
JOURNAL Mol. Vis. 8, 185-195. (2002)
MEDLINE 22103462
PUBMED 12107412

REFERENCE 2 (bases 1 to 3729)
AUTHORS Wistow,G.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD
20892-2740, USA

FEATURES
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BASE COUNT	1177 a	730 c	706 g	1116 t
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Query Match	1.88;	Score 550;	DB 9;	Length 3729;
Best Local Similarity	99.7%;	Pred. No. 5.8e-260;		
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Qy	301	ACTATTATTAAATGCAATCCTATATCTTAGGTATAGAAAGTTGATGATATACCTTTCTAC	360	
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GenCore version 5.1.6
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	377	1.3	1882	US-09-540-224-1	Sequence 1, Appl1
C 2	300	1.0	1910	US-09-457-066-36	Sequence 36, Appl1
C 3	119	0.4	33042	US-09-245-281-44	Sequence 44, Appl1
C 4	103	0.3	18596	US-09-318-448-11	Sequence 11, Appl1
C 5	94	0.3	50000	US-09-146-053-4	Sequence 4, Appl1
C 6	91	0.3	33042	US-09-245-281-44	Sequence 44, Appl1
C 7	91	0.3	152331	US-09-128-155-16	Sequence 16, Appl1
C 8	91	0.3	168575	US-09-426-290-1	Sequence 1, Appl1
C 9	91	0.3	176373	US-09-128-155-17	Sequence 17, Appl1
C 10	87	0.3	40328	US-08-742-185-102	Sequence 102, App
C 11	83	0.3	10754	US-08-966-958-1	Sequence 1, Appl1
C 12	83	0.3	10754	US-09-215-817-1	Sequence 1, Appl1
C 13	83	0.3	10754	US-09-342-353-1	Sequence 1, Appl1
C 14	80	0.3	6623	US-08-687-080-68	Sequence 68, Appl1
C 15	78	0.3	797	US-08-592-126-73	Sequence 73, Appl1
C 16	78	0.3	10607	US-08-078-090-3	Sequence 3, Appl1
C 17	73	0.2	731	US-09-288-143-38	Sequence 38, Appl1
C 18	71	0.2	98844	US-09-791-211-10	Sequence 10, Appl1
C 19	69	0.2	623	US-09-385-962-167	Sequence 167, App
C 20	64	0.2	87350	US-08-781-891-79	Sequence 79, Appl1
C 21	64	0.2	87543	US-09-791-211-3	Sequence 3, Appl1
C 22	64	0.2	168575	US-09-426-290-1	Sequence 1, Appl1
C 23	63	0.2	112132	US-09-397-787-117	Sequence 117, App
C 24	60	0.2	225	US-08-742-185-101	Sequence 101, App
C 25	59	0.2	43795	US-08-742-185-102	Sequence 102, App
C 26	57	0.2	40328	US-08-991-789A-246	Sequence 246, App
C 27	56	0.2	482		

28	56	0.2	482	4	US-09-062-451-246	Sequence 246, App
56	56	0.2	482	4	US-09-598-326-246	Sequence 246, App
30	56	0.2	6623	2	US-08-687-080-68	Sequence 68, Appl1
31	55	0.2	439	4	US-09-397-787-269	Sequence 269, App
32	55	0.2	7452	3	US-08-592-500-1	Sequence 1, Appl1
33	55	0.2	7452	3	US-08-195-006-1	Sequence 1, Appl1
34	55	0.2	7452	5	PCT-US94-07644A-1	Sequence 11, Appl1
35	55	0.2	18596	4	US-09-318-448-11	Sequence 3, Appl1
36	55	0.2	112132	4	US-09-741-150-3	Sequence 248, App
37	54	0.2	430	4	US-09-397-787-248	Sequence 420, App
38	54	0.2	573	4	US-09-385-962-420	Sequence 83, Appl1
39	54	0.2	2087	4	US-09-097-199-63	Sequence 61, Appl1
40	54	0.2	13187	4	US-09-422-936-61	Sequence 1, Appl1
41	54	0.2	72928	3	US-09-009-913-1	Sequence 25, Appl1
42	53	0.2	1523	1	US-07-795-859B-25	Sequence 25, Appl1
43	53	0.2	1523	1	US-08-457-616-25	Sequence 25, Appl1
44	53	0.2	4072	4	US-09-245-041-16	Sequence 16, Appl1
45	53	0.2	38844	4	US-09-734-675-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-540-224-1/c
Sequence 1, Application US/09540224
Patent No. 6468543
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CORRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (226)...(1338)
US-09-540-224-1
Query Match
Best Local Similarity 99.8%; Pred. No. 1.6e-112;
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1.3%; Score 377; DB 4; Length 1882;
225 AAAAAAAAAATTGATCTATATACATGACATGATATATTTCTGTGTGTTGTC 284
1638 AAAAAAAAAATTGATCTATATACATGACATGATATATTTCTGTGTGTTGTC 1579
285 AATATATACCTCAACATATATTAATGAATCCTATATTTAGGTATAGAGTGA 344
1578 AATATATACCTCAACATATATTAATGAATCCTATATTTAGGTATAGAGTGA 1519
345 TGATATACCTTCTACTTGCATGATGATTAACAAGAGCTGAGTCAACACT 404
1518 TGATATACCTTCTACTTGCATGATGATTAACAAGAGCTGAGTCAACACT 1459
405 TGTGTTCAATTCAGTGAAGCTAGTAGTATGTTGTTGTTGTTGTTGTTGTT 464
1458 TGTGTTCAATTCAGTGAAGCTAGTAGTATGTTGTTGTTGTTGTTGTTGTT 1399
465 ATTCACACCTCTTAATAAGGTTCTTCAAGCTTAATTAAGGTTCTTCAAGCT 524
1398 ATTCACACCTCTTAATAAGGTTCTTCAAGCTTAATTAAGGTTCTTCAAGCT 1339
525 TTATCAGAGTGTCTTGAAGTGCAGATCAATCAATGATGATGATGATGAT 584

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Db      1338  TTAATGAGTGTCTTGTAGCTGACATACATGATGATGATGATGATGAT 1279
Oy      585   GTCACTAGAGCATGCTTGTAGCTGACATGATGATGATGATGATGAT 644
Db      1278  GTCACTAGAGCATGCTTGTAGCTGACATGATGATGATGATGATGAT 1219
Oy      645   TAATACCT 652
Db      1218  TAATACCT 1211
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RESULT 2

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US-09-457-066-36/c
; Sequence 36, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVBSF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-457-066-36
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Query Match      1.0%; Score 300; DB 4; Length 1910;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      225  AAAAAAAAAATTTGATCTATATACATGACATGATATATTTCTGTGTGTTGTC 284
Db      1666  AAAAAAAAAATTTGATCTATATACATGACATGATATATTTCTGTGTGTTGTC 1607
Oy      285  ATATATACCTCAACACTATTATTAATGCAATCCTATATTTCTAGTATAGAAGTTGA 344
Db      1606  ATATATACCTCAACACTATTATTAATGCAATCCTATATTTCTAGTATAGAAGTTGA 1547
Oy      345  TGATATACCTTTCTACTTGCATGCGATTAACAAGAGGCTGAGACTGACAACT 404
Db      1546  TGATATACCTTTCTACTTGCATGCGATTAACAAGAGGCTGAGACTGACAACT 1487
Oy      405  TGTGTCTATTCATTCGACGCTAGTAGTAACTGTTGCTGTGAGAAAAGGCTCTCT 464
Db      1486  TGTGTCTATTCATTCGACGCTAGTAGTAACTGTTGCTGTGAGAAAAGGCTCTCT 1427
Oy      465  ATTCACGCTCTTAACATAAGGTTCTTCAGGCTTAATGAGATGTCACATCTC 524
Db      1426  ATTCACGCTCTTAACATAAGGTTCTTCAGGCTTAATGAGATGTCACATCTC 1367
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RESULT 3

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US-09-245-281-44
; Sequence 44, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
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; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/039,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 32042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-44
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Query Match      0.4%; Score 119; DB 4; Length 32042;
Best Local Similarity 100.0%; Pred. No. 7.9e-30;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      29612  CAGCACCATTTATTAATAGGAATCCTTCCCATTCCTTTCTCAGGTTGCA 29671
Db      13368  CAGCACCATTTATTAATAGGAATCCTTCCCATTCCTTTCTCAGGTTGCA 13427
Oy      29672  AAGATCAGATAGTTGATAGATAGCGGCAATTTCTGAGGCTCTGTTCTCCATTG 29730
Db      13428  AAGATCAGATAGTTGATAGATAGCGGCAATTTCTGAGGCTCTGTTCTCCATTG 13486
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RESULT 4

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US-09-318-448-11
; Sequence 11, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Steiros, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patenlin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-11
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Query Match      0.3%; Score 103; DB 4; Length 18596;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      29325  GTTCCCTGTTCACCTGATGATGTTCTTTGCTGTGCAAGACCTCTTAGTTAATTA 29384
Db      6706   GTTCCCTGTTCACCTGATGATGTTCTTTGCTGTGCAAGACCTCTTAGTTAATTA 6765
Oy      29385  GATCCCAATTTGTCAATTTGGCTTTGTGCCATTGCTTTGG 29427
Db      6766   GATCCCAATTTGTCAATTTGGCTTTGTGCCATTGCTTTGG 6808
```

RESULT 5

```
US-09-146-053-4
; Sequence 4, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
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; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-4

Query Match 0.3%; Score 94; DB 4; Length 50000;
Best Local Similarity 100.0%; Pred. No. 8e-22;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29497 TTTTATGGTTTGTAGTCTAACATTTAAGTCTTTAATCCATCTTGAATTAATTTTGTATA 29556
Db 27116 TTTTATGGTTTGTAGTCTAACATTTAAGTCTTTAATCCATCTTGAATTAATTTTGTATA 27175
QY 29557 AGGTGTAAGGAAGGATCCAGTTTCAGCTTTCTA 29590
Db 27176 AGGTGTAAGGAAGGATCCAGTTTCAGCTTTCTA 27209

RESULT 6
US-09-245-281-44/c
; Sequence 44, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 32042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-44

Query Match 0.3%; Score 91; DB 4; Length 32042;
Best Local Similarity 100.0%; Pred. No. 7.9e-21;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3644 GCAGGGTTGCAATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGA 3703
Db 15964 GCAGGGTTGCAATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGA 15905
QY 3704 GACAAAGAAGCCATTACATAATGGTTAAAG 3734
Db 15904 GACAAAGAAGCCATTACATAATGGTTAAAG 15874

RESULT 7
US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yanq
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 0.3%; Score 91; DB 3; Length 152331;
Best Local Similarity 100.0%; Pred. No. 6.1e-21;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28846 TGTGTCTTTATAGCAGCATGATTTAATCCTTTGGGTATATACCCAGTAATGGATGGC 28905
Db 53689 TGTGTCTTTATAGCAGCATGATTTAATCCTTTGGGTATATACCCAGTAATGGATGGC 53748
QY 28906 TGGTCAATGGTATTTCTAGTTCTAGATCC 28936
Db 53749 TGGTCAATGGTATTTCTAGTTCTAGATCC 53779

RESULT 8
US-09-426-290-1/c
; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 168575
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21181)...(21403)
; NAME/KEY: CDS
; LOCATION: (95252)...(95430)
; NAME/KEY: CDS
; LOCATION: (101753)...(101996)
; NAME/KEY: CDS
; LOCATION: (110324)...(110439)
; NAME/KEY: CDS
; LOCATION: (124058)...(124278)
; NAME/KEY: CDS
; LOCATION: (127009)...(127130)
; NAME/KEY: CDS
; LOCATION: (128910)...(129139)
US-09-426-290-1

Query Match 0.3%; Score 91; DB 4; Length 168575;
Best Local Similarity 100.0%; Pred. No. 6e-21;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3644 GCAGGGTTGCAATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGA 3703
Db 156614 GCAGGGTTGCAATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGA 156555
QY 3704 GACAAAGAAGCCATTACATAATGGTTAAAG 3734

Db 156554 GACAAAGAGGCCATTACATAATGGTAAAGG 156524

RESULT 9

US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 0.3%; Score 91; DB 3; Length 176373;

Best Local Similarity 100.0%; Pred. No. 5.9e-21;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28846 TGTGCTTTATAGCAGCATGATTATATCCCTTTGGGTATATACCCAGTAATGGGATGCC 28905

Db 56333 TGTGCTTTATAGCAGCATGATTATATCCCTTTGGGTATATACCCAGTAATGGGATGCC 56392

QY 28906 TGGGTCAAATGGTATTTCTAGTCTAGATCC 28936

Db 56393 TGGGTCAAATGGTATTTCTAGTCTAGATCC 56423

RESULT 10

US-08-742-185-102
; Sequence 102, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734

; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI94-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-102

Query Match 0.3%; Score 87; DB 3; Length 40328;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29612 CAGCACCATTTTAAATAGGAATCCTTTCCCATTCCTGTTTCTCAGGTTGTCA 29671

Db 17587 CAGCACCATTTTAAATAGGAATCCTTTCCCATTCCTGTTTCTCAGGTTGTCA 17646

QY 29672 AGATCAGATAGTTGTAGATATGCGGC 29698

Db 17647 AGATCAGATAGTTGTAGATATGCGGC 17673

RESULT 11

US-08-966-958-1/C
; Sequence 1, Application US/08966958
; Patent No. 5928908
; GENERAL INFORMATION:
; APPLICANT: Dunn, John
; APPLICANT: Randesi, Matthew
; TITLE OF INVENTION: METHODS FOR INTRODUCING UNIDIRECTIONAL
; TITLE OF INVENTION: DELETIONS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET: P.O. Box 5000
; CITY: Upton
; STATE: New York
; COUNTRY: US
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,958
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: AUI97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 344-3341
; TELEFAX: (516) 344-3729
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-966-958-1

Query Match 0.3%; Score 83; DB 2; Length 10754;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29612 CAGCACATTTATTAAATAGGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 29671
|||||
Db 10716 CAGCACATTTATTAAATAGGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 10657
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QY 29672 AGATCAGATAGTTGTAGATG 29694
|||||
Db 10656 AGATCAGATAGTTGTAGATG 10634
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RESULT 12

US-09-215-817-1/c

; Sequence 1, Application US/09215817

; Patent No. 5968786

; GENERAL INFORMATION:

; APPLICANT: Dunn, John

; APPLICANT: Randesi, Matthew

; TITLE OF INVENTION: METHODS FOR INTRODUCING UNIDIRECTIONAL

; TITLE OF INVENTION: DELETIONS

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brookhaven National Laboratory

; STREET: P.O. Box 5000

; CITY: Upton

; STATE: New York

; COUNTRY: US

; ZIP: 11973

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/215,817

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/966,958

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bogosian, Margaret

; REGISTRATION NUMBER: 25,324

; REFERENCE/DOCKET NUMBER: AUI97-14

; TELEPHONE: (516) 344-3341

; TELEFAX: (516) 344-3729

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10754 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-09-215-817-1

Query Match 0.3%; Score 83; DB 2; Length 10754;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29612 CAGCACATTTATTAAATAGGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 29671
|||||
Db 10716 CAGCACATTTATTAAATAGGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 10657
|||||
QY 29672 AGATCAGATAGTTGTAGATG 29694
|||||
Db 10656 AGATCAGATAGTTGTAGATG 10634
|||||

RESULT 13

US-09-342-353-1/c

; Sequence 1, Application US/09342353

; Patent No. 6248569

; GENERAL INFORMATION:

; APPLICANT: Dunn, John

; TITLE OF INVENTION: METHOD FOR INTRODUCING UNIDIRECTIONAL NESTED DELETIONS

; FILE REFERENCE: CIP OF U.S. Application 08/966,958

; CURRENT APPLICATION NUMBER: US/09/342,353

; CURRENT FILING DATE: 1999-06-29

; EARLIER APPLICATION NUMBER: 08/966,958

; EARLIER FILING DATE: 1997-11-10

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 10754

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-342-353-1

Query Match 0.3%; Score 83; DB 4; Length 10754;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29612 CAGCACATTTATTAAATAGGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 29671
|||||
Db 10716 CAGCACATTTATTAAATAGGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 10657
|||||
QY 29672 AGATCAGATAGTTGTAGATG 29694
|||||
Db 10656 AGATCAGATAGTTGTAGATG 10634
|||||

RESULT 14

US-08-687-080-68/c

; Sequence 68, Application US/08687080

; Patent No. 5968786

; GENERAL INFORMATION:

; APPLICANT: Gregory Dolganov

; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,080

; FILING DATE: 17-JUL-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/592,126

; FILING DATE: 26-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 4600-0111.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6623 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 3' END OF INTRON 5 OF RAD50 GENOMIC
; INDIVIDUAL ISOLATE: SEQUENCE
; US-08-687-080-68

Query Match 0.3%; Score 80; DB 2; Length 6623;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28846 TGTGCTTTATACGACGATGTTTATAATCCCTTTGGGTATATACCCAGTAAATGGGATGGC 28905
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3700 TGTGCTTTATACGACGATGTTTATAATCCCTTTGGGTATATACCCAGTAAATGGGATGGC 3641
QY 28906 TGGGTCAATGGTATTCTTA 28925
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3640 TGGGTCAATGGTATTCTTA 3621

RESULT 15

US-08-592-126-73
; Sequence 73, Application US/08592126
; Patent No. 5821091

; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.126
; FILING DATE:

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 73:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 797 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: G248b.seq

; US-08-592-126-73

Query Match 0.3%; Score 78; DB 1; Length 797;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28434 GTTACATATGATACATGCGCTGCTGCTGCGACCCATTAACTCGTCATTAAACA 28493
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GTTACATATGATACATGCGCTGCTGCTGCGACCCATTAACTCGTCATTAAACA 720

QY 28494 TTAGGTATATCTCTTAAT 28511
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 TTAGGTATATCTCTTAAT 738
Search completed: July 8, 2003, 04:39:42
Job time : 908 secs

QY	241	CTATATACACATAGACATGAATATATATTTCTGTGTGTGTGTGTGCATATATAACTCCAAC	300
DB	241	CTATATACACATAGACATGAATATATATTTCTGTGTGTGTGTGTGCATATATAACTCCAAC	300
QY	301	ACTATTATTAATCGAATCCCTATATCTTAGGTATAGAACTTGATGATATACCTTTCTAC	360
DB	301	ACTATTATTAATCGAATCCCTATATCTTAGGTATAGAACTTGATGATATACCTTTCTAC	360
QY	361	TTGCCATGGCAATTAAACAAGCAAGCGCTGAGACTCAGCAACACACTTGTTTCATTGCAATG	420
DB	361	TTGCCATGGCAATTAAACAAGCAAGCGCTGAGACTCAGCAACACACTTGTTTCATTGCAATG	420
QY	421	CAGGCTAGTAGTAAGTTGGTTGCTGTAGGAAAAGGCTCTCTTTATCTCACCCCTCTTAA	480
DB	421	CAGGCTAGTAGTAAGTTGGTTGCTGTAGGAAAAGGCTCTCTTTATCTCACCCCTCTTAA	480
QY	481	ACTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTTATCAGAGGTGCTT	540
DB	481	ACTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTTATCAGAGGTGCTT	540
QY	541	GAGCTGCAGATACAAATCACATCGTTCAATGGTGATCCAACTGGAGTGTCAACTAGAGCCATG	600
DB	541	GAGCTGCAGATACAAATCACATCGTTCAATGGTGATCCAACTGGAGTGTCAACTAGAGCCATG	600
QY	601	GTCTTAGCTCTACCCCTCTTCTGATGTGGCCAGGCTCAAACTGTAATACCTAGGACAAG	660
DB	601	GTCTTAGCTCTACCCCTCTTCTGATGTGGCCAGGCTCAAACTGTAATACCTAGGACAAG	660
QY	661	AAGCACATCTCCTGTTAGAAAGCCTTTGGAGTTCAACTCAGTCAAGTGCACCTTACTTAT	720
DB	661	AAGCACATCTCCTGTTAGAAAGCCTTTGGAGTTCAACTCAGTCAAGTGCACCTTACTTAT	720
QY	721	TACCTTTTGCACAACTAGTTCTTAGCCCTTTGAGAACCCACAGAACTATGGGCTTGCT	780
DB	721	TACCTTTTGCACAACTAGTTCTTAGCCCTTTGAGAACCCACAGAACTATGGGCTTGCT	780
QY	781	ATTAGAATGCACAGCTTCTATTAGAATGTACACATTTTCAAAATAATGACTCCCTGAA	840
DB	781	ATTAGAATGCACAGCTTCTATTAGAATGTACACATTTTCAAAATAATGACTCCCTGAA	840
QY	841	GTGGAGGAATCAATGTATCCAGAGTAATGCCCAAGCATTAACCTTACCTGAAGTACCCAGAT	900
DB	841	GTGGAGGAATCAATGTATCCAGAGTAATGCCCAAGCATTAACCTTACCTGAAGTACCCAGAT	900
QY	901	GATTTCAATGTCTTTAGCAGGTATTTAATAGCTTTCTAAGGCCCTGCTTTGGGCCAA	960
DB	901	GATTTCAATGTCTTTAGCAGGTATTTAATAGCTTTCTAAGGCCCTGCTTTGGGCCAA	960
QY	961	GTACTGTTCCAAATATTATCGTAAAGATCCTTCTGACCAAGGATGTGTTATAGATGAAT	1020
DB	961	GTACTGTTCCAAATATTATCGTAAAGATCCTTCTGACCAAGGATGTGTTATAGATGAAT	1020
QY	1021	ACAATCTTGAGCATATTTATAGCATGGAGAGGAAATGAATCAACCATGAATAAATA	1080
DB	1021	ACAATCTTGAGCATATTTATAGCATGGAGAGGAAATGAATCAACCATGAATAAATA	1080
QY	1081	TGCTGGTATATCTAAATCTTTTGGTTGAAGTAAACATGTTGCCCTGAGTTGCTGGCAAG	1140
DB	1081	TGCTGGTATATCTAAATCTTTTGGTTGAAGTAAACATGTTGCCCTGAGTTGCTGGCAAG	1140
QY	1141	ATGCCCGAACAGGAACAGCTCTGCTCTGCAGTTTCCCAGCGAGATCAATGAGAGCGCGG	1200
DB	1141	ATGCCCGAACAGGAACAGCTCTGCTCTGCAGTTTCCCAGCGAGATCAATGAGAGCGCGG	1200
QY	1201	TGATTTCTCCATTTCCCAACTGAGGTACCCAGTTCAATCTCATGGGACTGGTTAGACATG	1260
DB	1201	TGATTTCTCCATTTCCCAACTGAGGTACCCAGTTCAATCTCATGGGACTGGTTAGACATG	1260
QY	1261	GGTGCACCCACGGAAGGCTGAGCTGAGCAGGTTGGGCTGCTCCCTCAGCCGGAAGTGC	1320
DB	1261	GGTGCACCCACGGAAGGCTGAGCTGAGCAGGTTGGGCTGCTCCCTCAGCCGGAAGTGC	1320
QY	1321	AAGGGGTGGGGATCTCTCTTCCCCAGCCAAAGGAAGCCATGAGAGACTGTACCAAGGAG	1380

[illegible]

Db	2401	CAAGAGATCAAACTCTCCAGCAAGGGAACAAAACCAAGATGGAGAATGAGTTGAGG	2460	3541	GTGCTGTATTTCAGGAGCCCATCTCACATGAAAAGACACATAGGCTCAAAATAAAGGG	3600	
Qy	2461	AATTGACAGAGTAGGCTTCAGAGAGTGGGTAAATAACAAACTCTCTCGAGCTAAAGAGC	2520	Db	3541	GTGCTGTATTTCAGGAGCCCATCTCACATGAAAAGACACATAGGCTCAAAATAAAGGG	3600
Db	2461	AATTGACAGAGTAGGCTTCAGAGAGTGGGTAAATAACAAACTCTCTCGAGCTAAAGAGC	2520	Qy	3601	ATGGAGAGATTTACCAAGTAAATGTAAGAAAACAAAAAAGCAGGGGTGCAATCCT	3660
Qy	2521	ATGTTCTAACCCCAATCAAGGAAGCTAAGAACCTTGAAAAAGGTAGATTGCTAA	2580	Db	3601	ATGGAGAGATTTACCAAGTAAATGTAAGAAAACAAAAAAGCAGGGGTGCAATCCT	3660
Db	2521	ATGTTCTAACCCCAATCAAGGAAGCTAAGAACCTTGAAAAAGGTAGATTGCTAA	2580	Qy	3661	AGTCTCTGATTAACACAGACTTTAAACCAACAAGATCAAAAGAGACAAAGAGCCATTA	3720
Qy	2581	CTAGAATAATCAGTGTAGAGAGACATAAATGACCTGATGGAGCTGAAAAAGCAAGAC	2640	Db	3661	AGTCTCTGATTAACACAGACTTTAAACCAACAAGATCAAAAGAGACAAAGAGCCATTA	3720
Db	2581	CTAGAATAATCAGTGTAGAGAGACATAAATGACCTGATGGAGCTGAAAAAGCAAGAC	2640	Qy	3721	CATAAATGCTTAAGGCATCAATGGAACAAGAGCTAACTATCCTAAATATACATGCACC	3780
Qy	2641	AAGAACTTCATGAAGCATACACAGCTTCAATAGCCAAATCGATCAAGCAGAGAGAAAGGA	2700	Db	3721	CATAAATGCTTAAGGCATCAATGGAACAAGAGCTAACTATCCTAAATATACATGCACC	3780
Db	2641	AAGAACTTCATGAAGCATACACAGCTTCAATAGCCAAATCGATCAAGCAGAGAGAAAGGA	2700	Qy	3781	CAATACAGGAGCAGCCAGATTCATAAAGCAAGTCTTTAGAGACCTACAAGAGAGACTTTGA	3840
Qy	2701	TATCAGTGTATGAAGATCAAAATTAATAAAGAAAGTGAGAGACAGATTCAGAAAAA	2760	Db	3781	CAATACAGGAGCAGCCAGATTCATAAAGCAAGTCTTTAGAGACCTACAAGAGAGACTTTGA	3840
Db	2701	TATCAGTGTATGAAGATCAAAATTAATAAAGAAAGTGAGAGACAGATTCAGAAAAA	2760	Qy	3841	CTCCACACATAATAGTGGAGTCTAAATAAATAATAGACACTTTAACACCCACCTGCC	3900
Qy	2761	GAGTGAAGAAACACACAAAGCTTCAAGAAATTTATGGGACTATGTAAAAAGACCAATC	2820	Db	3841	CTCCACACATAATAGTGGAGTCTAAATAAATAATAGACACTTTAACACCCACCTGCC	3900
Db	2761	GAGTGAAGAAACACACAAAGCTTCAAGAAATTTATGGGACTATGTAAAAAGACCAATC	2820	Qy	3901	AATATTAGGAGATCAATGAGACAGAAAAATTAACAAGATATCCAGGAGTTGAACCTGAGC	3960
Qy	2821	TACATTTGATTTGGTGTCCCCAAAGTGTGGGAGATGGAATCAAGTTGGAAGAACTC	2880	Db	3901	AATATTAGGAGATCAATGAGACAGAAAAATTAACAAGATATCCAGGAGTTGAACCTGAGC	3960
Db	2821	TACATTTGATTTGGTGTCCCCAAAGTGTGGGAGATGGAATCAAGTTGGAAGAACTC	2880	Qy	3961	TCGGACCAAGCGGACCTAATAGATATCTACAGAACTCCCCACCCCAAAATCAACAGAA	4020
Qy	2881	TTGAGGATATATCCAGGAGAAATTCOCCTATATCAGGCGAGCCCAACATTCAAATTC	2940	Db	3961	TCGGACCAAGCGGACCTAATAGATATCTACAGAACTCCCCACCCCAAAATCAACAGAA	4020
Db	2941	GGAAATATGAGAACACATTAAGATATCTCTGAGAGAAACAAATCCCAAGACACATAAT	3000	Qy	4021	TACACTCTCTCAGCATCATATACCTATTTTAAATTTGACCATCTAATTTTAAAGTAA	4080
Qy	3001	CTTCAGATTCACCAAGGTTGAAATGAAGAAAAAATGTTAAGGCGAGCCAGAGAGAAGG	3060	Db	4021	TACACTCTCTCAGCATCATATACCTATTTTAAATTTGACCATCTAATTTTAAAGTAA	4080
Db	3001	CTTCAGATTCACCAAGGTTGAAATGAAGAAAAAATGTTAAGGCGAGCCAGAGAGAAGG	3060	Qy	4081	AACACTCTCAGCAAAATGCAAAAAGACAGAAATCCTTAACAAACAGTCTCTCAGACTACAG	4140
Qy	3061	TTGGGTTACCCCAAAAGGAGCCAAATCAGACTAACAGCGGATCTCCCGGAGAAACCT	3120	Db	4081	AACACTCTCAGCAAAATGCAAAAAGACAGAAATCCTTAACAAACAGTCTCTCAGACTACAG	4140
Db	3061	TTGGGTTACCCCAAAAGGAGCCAAATCAGACTAACAGCGGATCTCCCGGAGAAACCT	3120	Qy	4141	TGCATCTATTAGAACTCAGAAATTAAGAAACTCCTCAAAATCAACAACTACATCGAA	4200
Qy	3121	ACAGCCAGAGAGAGTGAGGCGCAATATTCACATCTTTAAGAAATATATTTTCAACC	3180	Db	4141	TGCATCTATTAGAACTCAGAAATTAAGAAACTCCTCAAAATCAACAACTACATCGAA	4200
Db	3121	ACAGCCAGAGAGAGTGAGGCGCAATATTCACATCTTTAAGAAATATATTTTCAACC	3180	Qy	4201	ACTGAACAACCTGCTCTGATGACTACTGGGTAAATTAACAAATGAAGGCAAAATATAA	4260
Qy	3181	CAGAAATTTATATCCAGCCAAACCAAGCTTCCCTAAGTGAAGGAGAAATAAATCCTCTAC	3240	Db	4201	ACTGAACAACCTGCTCTGATGACTACTGGGTAAATTAACAAATGAAGGCAAAATATAA	4260
Db	3181	CAGAAATTTATATCCAGCCAAACCAAGCTTCCCTAAGTGAAGGAGAAATAAATCCTCTAC	3240	Qy	4261	GATGTTCTTTGAAACCAATGAGAAACAAAGACACAAATGTACCAGAAATCTCTGGGCAATTT	4320
Qy	3241	AGAGAACCAATGCTGACAGATTTTGTACACACAGGCTGCTTACAGAGAGCTCTGA	3300	Db	4261	GATGTTCTTTGAAACCAATGAGAAACAAAGACACAAATGTACCAGAAATCTCTGGGCAATTT	4320
Db	3241	AGAGAACCAATGCTGACAGATTTTGTACACACAGGCTGCTTACAGAGAGCTCTGA	3300	Qy	4321	TAAAGCAGTGTAGAGGGAAATTTATAGCACTAGATGCTTACAGAGAAAGCAGGAAAT	4380
Qy	3301	AGGAGCACCACATGGAAGGACAACTGGTACCCAGCCACTGCAAAAACATCCCAATTT	3360	Db	4321	TAAAGCAGTGTAGAGGGAAATTTATAGCACTAGATGCTTACAGAGAAAGCAGGAAAT	4380
Db	3301	AGGAGCACCACATGGAAGGACAACTGGTACCCAGCCACTGCAAAAACATCCCAATTT	3360	Qy	4381	ATCTTAAATAGACACCTTTAATCAATCAATTAAGAAACTAGAGAAAGAGCAACAAA	4440
Qy	3361	GTAAGACCAATGATGTATGAAGAAAGTGCATCACTAAGGCAAAATAAACAGCTAG	3420	Db	4381	ATCTTAAATAGACACCTTTAATCAATCAATTAAGAAACTAGAGAAAGAGCAACAAA	4440
Db	3361	GTAAGACCAATGATGTATGAAGAAAGTGCATCACTAAGGCAAAATAAACAGCTAG	3420	Qy	4441	TTCAAAAGCTTAGCAGAGACAAAGAAATTAAGTACAGAGCAGAACTGAGAGGAGATAGA	4500
Qy	3421	TGTCATATGCGAGGATCAAAATCACACATTAATAATTAACCTTAAATGTAATGGGCT	3480	Db	4441	TTCAAAAGCTTAGCAGAGACAAAGAAATTAAGTACAGAGCAGAACTGAGAGGAGATAGA	4500
Db	3421	TGTCATATGCGAGGATCAAAATCACACATTAATAATTAACCTTAAATGTAATGGGCT	3480	Qy	4501	GACACAAAAAGCCCTTCAAAATAATCAATGAATCCAGGAGCTGGTTTTTTGAAAGATCA	4560
Qy	3481	AAATTCCTCAATTAAGACACAGACTGGCAATTTGGATTAAGAGTCAAGACCCATCAGT	3540	Db	4501	GACACAAAAAGCCCTTCAAAATAATCAATGAATCCAGGAGCTGGTTTTTTGAAAGATCA	4560
Db	3481	AAATTCCTCAATTAAGACACAGACTGGCAATTTGGATTAAGAGTCAAGACCCATCAGT	3540	Qy	4561	GCAAAATAGACCCTAGACAGACTTAATAAGAGAAAGAGAGAGAAATCAAGAGATGC	4620
				Db	4561	GCAAAATAGACCCTAGACAGACTTAATAAGAGAAAGAGAGAGAAATCAAGAGATGC	4620

QY	4621	AAATAAAATGATAAAGGGGATATACACCGATCCACAGAAATACAAACTATTATCAG	4680		5701	AGGCCCTTGTCAAAATTCACAGCCCTCATGCTAAAAATTCAGTAAACTAGGTATCG	5760		
Db	4621	AAATAAAATGATAAAGGGGATATACACCGATCCACAGAAATACAAACTATTATCAG	4680		QY	5761	ATGGGAATGTATCTCAAATAATAAGAGCTATTATACAAACCCACAGCCAATATCATACT	5820	
QY	4681	AGAAATATTAAACACCTCTATGCAAAATAAAGAGTAACTAGAAATCTAGAAATGGATAAAT	4740		Db	5761	ATGGGAATGTATCTCAAATAATAAGAGCTATTATACAAACCCACAGCCAATATCATACT	5820	
Db	4681	AGAAATATTAAACACCTCTATGCAAAATAAAGAGTAACTAGAAATCTAGAAATGGATAAAT	4740		QY	5821	GAATGGGCAAAACTGGGAAGCAATCCCTTTGAGAACTGGCACAAGCAAGGATGCCCTCT	5880	
QY	4741	CTGGACACATATGTAGCCCTGTATGGACCTTTGGGGACAGAAACAAAGGGGTGAATGCA	4800		Db	5821	GAATGGGCAAAACTGGGAAGCAATCCCTTTGAGAACTGGCACAAGCAAGGATGCCCTCT	5880	
Db	4741	CTGGACACATATGTAGCCCTGTATGGACCTTTGGGGACAGAAACAAAGGGGTGAATGCA	4800		QY	5881	CTCACCACCTCTTATTCAGATACTATTGGAAGTCTTGCCAGCGGCAATCAGGCAATAGAA	5940	
QY	4801	GAATAAAAGACAAAGACAAAAGAGTATGTTTGGAACTAGGGGTAGGGGGCAACTTGCC	4860		Db	5881	CTCACCACCTCTTATTCAGATACTATTGGAAGTCTTGCCAGCGGCAATCAGGCAATAGAA	5940	
Db	4801	GAATAAAAGACAAAGACAAAAGAGTATGTTTGGAACTAGGGGTAGGGGGCAACTTGCC	4860		QY	5941	AGAAATAAAGGTATTCAAATAGAAAGAGAGAAAGTCAATTTGCTCTGTTTGCAGATGA	6000	
QY	4861	TCTAATGGACAGGGCCCTGAGCTTTACACCACTCTCTGATTTATTAGGCAAAAGAGAT	4920		Db	5941	AGAAATAAAGGTATTCAAATAGAAAGAGAGAAAGTCAATTTGCTCTGTTTGCAGATGA	6000	
Db	4861	TCTAATGGACAGGGCCCTGAGCTTTACACCACTCTCTGATTTATTAGGCAAAAGAGAT	4920		QY	6001	CATGTTTGTATATTAGAAAACCCCATCGTCTCAGGCCAAAAACTCCTTTAAGCTGATAAG	6060	
QY	4921	AGCGAGAGGTGAGTTGGAAGAAGAGTCAAGCTGTTAGGTCAGAGTAGGCTGCAAGAC	4980		Db	6001	CATGTTTGTATATTAGAAAACCCCATCGTCTCAGGCCAAAAACTCCTTTAAGCTGATAAG	6060	
Db	4921	AGCGAGAGGTGAGTTGGAAGAAGAGTCAAGCTGTTAGGTCAGAGTAGGCTGCAAGAC	4980		QY	6061	CAACTTTCAGCAAAAGTCTCAGGACACAAAATCAATGTGCAAAAATCACAAGCATTTCTATA	6120	
QY	4981	TGCATTCTCAACAAATAGGCTCTAGATGTCACAGTAGATAACCTCAAGAGCCAGTGCC	5040		Db	6061	CAACTTTCAGCAAAAGTCTCAGGACACAAAATCAATGTGCAAAAATCACAAGCATTTCTATA	6120	
Db	4981	TGCATTCTCAACAAATAGGCTCTAGATGTCACAGTAGATAACCTCAAGAGCCAGTGCC	5040		QY	6121	CGCCCAATATAGCAAAACAGAGAGCCCAATCATGATGATGAACCTCTCATTCACAAATTCGCTAC	6180	
QY	5041	AGGGAGTGATGCCCTCAGCAAACTTCTAGGGCAGGCACAGAAAGTAAAGTTTGGCCACAT	5100		Db	6121	CGCCCAATATAGCAAAACAGAGAGCCCAATCATGATGATGAACCTCTCATTCACAAATTCGCTAC	6180	
Db	5041	AGGGAGTGATGCCCTCAGCAAACTTCTAGGGCAGGCACAGAAAGTAAAGTTTGGCCACAT	5100		QY	6181	AAAGAGAATAAATACCTAGGAATACACTTACAAAGGACAGCTAGGAACTCTTCAAGGA	6240	
QY	5101	TCGTATTCCAGATAAACAGATTGCTGTTGATCAAGTAGCCCTCCAGTGGAATGCTGAGT	5160		Db	6181	AAAGAGAATAAATACCTAGGAATACACTTACAAAGGACAGCTAGGAACTCTTCAAGGA	6240	
Db	5101	TCGTATTCCAGATAAACAGATTGCTGTTGATCAAGTAGCCCTCCAGTGGAATGCTGAGT	5160		QY	6241	GACTTACAAACACCTGATCAAGGAATTAAGAGAGACACAAATGGAAGCAATTCCTCC	6300	
QY	5161	TGTCATGATCCCTTTGGCCTTTTGGCTTCCCAAAACACATACACCTCTCAAGACTAAA	5220		Db	6241	GACTTACAAACACCTGATCAAGGAATTAAGAGAGACACAAATGGAAGCAATTCCTCC	6300	
Db	5161	TGTCATGATCCCTTTGGCCTTTTGGCTTCCCAAAACACATACACCTCTCAAGACTAAA	5220		QY	6301	ATGCTCACAGATAGTAAGAAATCATGAAATGCATCTGCCCCAAAGTAAATATAGATTTC	6360	
QY	5221	CCAGGAAGAGTCAATCCCTCAATATACCACTACAAAGTCTCAAAATTAAGAGCAATAT	5280		Db	6301	ATGCTCACAGATAGTAAGAAATCATGAAATGCATCTGCCCCAAAGTAAATATAGATTTC	6360	
Db	5221	CCAGGAAGAGTCAATCCCTCAATATACCACTACAAAGTCTCAAAATTAAGAGCAATAT	5280		QY	6361	ATGCTTACCCCATCAAGCTACCACTTGTCTTTCACAGAAATGGAAGCAAACTTTA	6420	
QY	5281	TGATAGCTTACCAACCAAAAAAGTCCAGGACAGACGGATTCACAGCCCAATTTCTACCA	5340		Db	6361	ATGCTTACCCCATCAAGCTACCACTTGTCTTTCACAGAAATGGAAGCAAACTTTA	6420	
Db	5281	TGATAGCTTACCAACCAAAAAAGTCCAGGACAGACGGATTCACAGCCCAATTTCTACCA	5340		QY	6421	AAATTCATATGGAACCAAAAAAGAGCCCAAGAGCCCAAGCAATCTTAAGCAAAAGNA	6480	
QY	5341	GAGGTACAAAGAGAGCTGGTACTATTCTTCTGAAACTATTCCTCAAAATTAAGAAATGG	5400		Db	6421	AAATTCATATGGAACCAAAAAAGAGCCCAAGAGCCCAAGCAATCTTAAGCAAAAGNA	6480	
Db	5341	GAGGTACAAAGAGAGCTGGTACTATTCTTCTGAAACTATTCCTCAAAATTAAGAAATGG	5400		QY	6481	CAAAAGCTGGAGTATCATGCTACCTGACTTAAACTATATTAAGGCTACAGTAACCA	6540	
QY	5401	GAATCCTCCTAACTCAATTTACGAGGCGAGCATCATCTGATACCAAAACCTACGAGTG	5460		Db	6481	CAAAAGCTGGAGTATCATGCTACCTGACTTAAACTATATTAAGGCTACAGTAACCA	6540	
Db	5401	GAATCCTCCTAACTCAATTTACGAGGCGAGCATCATCTGATACCAAAACCTACGAGTG	5460		QY	6541	AACTGCATGGTACTGGTACCAAAACAGATATATACCAATGGAAGCAAGACAGACCTC	6600	
QY	5461	ACACAACAAAAAGAGAAATTTACGCGCCCATATCCCTGATGAACATTTGATGTAATTC	5520		Db	6541	AACTGCATGGTACTGGTACCAAAACAGATATATACCAATGGAAGCAAGACAGACCTC	6600	
Db	5461	ACACAACAAAAAGAGAAATTTACGCGCCCATATCCCTGATGAACATTTGATGTAATTC	5520		QY	6601	AGAAATACACTGCAATCTACATCCATCTGATCTTTGACAAACCTGACAAAAACAGCA	6660	
QY	5521	TCAATAAATACTGCAACCAAAATCCAGCAGCAGCATCAAAAGCTTTATCTACCATGATC	5580		Db	6601	AGAAATACACTGCAATCTACATCCATCTGATCTTTGACAAACCTGACAAAAACAGCA	6660	
Db	5521	TCAATAAATACTGCAACCAAAATCCAGCAGCAGCATCAAAAGCTTTATCTACCATGATC	5580		QY	6661	TGGAAGAGGATTCCTCTATTAAATGAGTGTGGAAAACTGGCTAGCCATATGCAGA	6720	
QY	5581	AAATTTGGGCTCATCCTGGGATGCAAGGCTGTTTCAAAATATGCAAAATCAATTAATGTAG	5640		Db	6661	TGGAAGAGGATTCCTCTATTAAATGAGTGTGGAAAACTGGCTAGCCATATGCAGA	6720	
Db	5581	AAATTTGGGCTCATCCTGGGATGCAAGGCTGTTTCAAAATATGCAAAATCAATTAATGTAG	5640		QY	6721	AACTGAAACTGGATGCCCTTCTTACACCTTATACAAAGTTAACTCAAGATGAATAAA	6780	
QY	5641	GCCATCACATAAAGACCAATGACAAAAACCAATGATTTATCTCAATAGATGAGAAA	5700		Db	6721	AACTGAAACTGGATGCCCTTCTTACACCTTATACAAAGTTAACTCAAGATGAATAAA	6780	
Db	5641	GCCATCACATAAAGACCAATGACAAAAACCAATGATTTATCTCAATAGATGAGAAA	5700		QY	6781	GACTTAATATTAAGACATAAAACCATAAACCCAGAGAAACCTTAGGCATACCATTC	6840	
QY	5701	AGGCCCTTTGTCAAAATTCACAGCCCTTCATGCTAAAAATTCCTCAGTAAACTAGGTATCG	5760						

Db 6781 GACTTAATATAGACATAAAACCATAAAAAACCAGAAAGAAACCTTAGGCCAATACCATTTC 6840
QY 6841 AGGATATGGACATGGGCAAGACCTTCATGACTAAAACACCAAAAGCAATGGCAACAAAG 6900
Db 6841 AGGATATGGACATGGGCAAGACCTTCATGACTAAAACACCAAAAGCAATGGCAACAAAG 6900
QY 6901 CCAAAATAGACAAGTGGGATCTGATTAAACTATAGAGCTTCTGGACAGCAAAAAAAACT 6960
Db 6901 CCAAAATAGACAAGTGGGATCTGATTAAACTATAGAGCTTCTGGACAGCAAAAAAAACT 6960
QY 6961 GTCATCAGAGTGAACAAGCAACCTACAGAATGGGAGAAATTTTGGCAATCTATCGATCT 7020
Db 6961 GTCATCAGAGTGAACAAGCAACCTACAGAATGGGAGAAATTTTGGCAATCTATCGATCT 7020
QY 7021 GACAAAGCTTAATATCCAGAGATCTACGAAGAACTTAAACAAATTTACAAGAAAAAACA 7080
Db 7021 GACAAAGCTTAATATCCAGAGATCTACGAAGAACTTAAACAAATTTACAAGAAAAAACA 7080
QY 7081 ACCCGGTCAAAATATGGCAAGGATATGACGACAGACCTTCTCAAAAAGAACATTTATG 7140
Db 7081 ACCCGGTCAAAATATGGCAAGGATATGACGACAGACCTTCTCAAAAAGAACATTTATG 7140
QY 7141 CAGCAACAAACATATGAAAAAACCCTCATCATCTGCTGTAGAGAAATGCAAAACA 7200
Db 7141 CAGCAACAAACATATGAAAAAACCCTCATCATCTGCTGTAGAGAAATGCAAAACA 7200
QY 7201 AAACACAGTGCATACCATCTCATGCTAGTGTAGAACTTCAAAAAGTACAGGAA 7260
Db 7201 AAACACAGTGCATACCATCTCATGCTAGTGTAGAACTTCAAAAAGTACAGGAA 7260
QY 7261 ACACAAATGCTGGAGAGATGTGGAGAAATAGGAACACTTTCCACTGTTGGTGGGAAT 7320
Db 7261 ACACAAATGCTGGAGAGATGTGGAGAAATAGGAACACTTTCCACTGTTGGTGGGAAT 7320
QY 7321 GTAAATAGTTCACCAATGTGGAGAGAGTGTGGAGAAATAGGAACACTTTCCACTGTTGGTGGGAAT 7380
Db 7321 GTAAATAGTTCACCAATGTGGAGAGAGTGTGGAGAAATAGGAACACTTTCCACTGTTGGTGGGAAT 7380
QY 7381 AAATATCATTTGACCCAGCAATCCCATTTACTGAGTATATACCAAGAAATATAATCAT 7440
Db 7381 AAATATCATTTGACCCAGCAATCCCATTTACTGAGTATATACCAAGAAATATAATCAT 7440
QY 7441 TCTATTATAAGACACATGCACATATGTTTATGTCAGCACTGATCAATAGCAAGA 7500
Db 7441 TCTATTATAAGACACATGCACATATGTTTATGTCAGCACTGATCAATAGCAAGA 7500
QY 7501 CTTGGAACCAACCAATGTCATCAGTATAGTGTGATTAAGAAACATGGCACATAT 7560
Db 7501 CTTGGAACCAACCAATGTCATCAGTATAGTGTGATTAAGAAACATGGCACATAT 7560
QY 7561 ACACATGAATATCTATGACCCATATAAAGGATGAGTTCATGCTCTTGGCAGAGATATG 7620
Db 7561 ACACATGAATATCTATGACCCATATAAAGGATGAGTTCATGCTCTTGGCAGAGATATG 7620
QY 7621 GATGAAGTGAACCAATCTCAGCAAACTTAACACAGAACAGAAACCAACACCA 7680
Db 7621 GATGAAGTGAACCAATCTCAGCAAACTTAACACAGAACAGAAACCAACACCA 7680
QY 7681 CATGTTCTCACTTGTAGTGGAGTGTGAACATGAGAGACATGGACAGGGGGAA 7740
Db 7681 CATGTTCTCACTTGTAGTGGAGTGTGAACATGAGAGACATGGACAGGGGGAA 7740
QY 7741 CATCACACACAGGTCCTGTTGTTGGTGGGAGTATAGGAGGATAGCATTTAGGAGAA 7800
Db 7741 CATCACACACAGGTCCTGTTGTTGGTGGGAGTATAGGAGGATAGCATTTAGGAGAA 7800
QY 7801 ATACCTAATGTAGATGACGGTGTGATGGTGCAGCAAGCCACCATGGCACATGTATACCT 7860
Db 7801 ATACCTAATGTAGATGACGGTGTGATGGTGCAGCAAGCCACCATGGCACATGTATACCT 7860
QY 7861 ATGTAAACAAACCTGCACATCTGCACATGTACCCCAACACTTAAAGTATTAAAAAATA 7920
Db 7861 ATGTAAACAAACCTGCACATCTGCACATGTACCCCAACACTTAAAGTATTAAAAAATA 7920

QY 7921 CACACAACATGTTGCCCTGATGAAGGTCATTTAGTGCCCATAAATAAGTAAATGTGTTTT 7980
Db 7921 CACACAACATGTTGCCCTGATGAAGGTCATTTAGTGCCCATAAATAAGTAAATGTGTTTT 7980
QY 7981 ATGTTTTTATATATTTGTTAAACATATATATATCTTTTACCATTAAACAAATCAGGTTCC 8040
Db 7981 ATGTTTTTATATATTTGTTAAACATATATATATCTTTTACCATTAAACAAATCAGGTTCC 8040
QY 8041 ACTAAAATCTTTGTATATTAATACCTGTGTATCAATACAGCATTTCTTAAATCAATAAGT 8100
Db 8041 ACTAAAATCTTTGTATATTAATACCTGTGTATCAATACAGCATTTCTTAAATCAATAAGT 8100
QY 8101 ATATCATTTAATTTTAAATTCATAGTTTAAACATAATTTCTTAAATTAGTAGTTAAATA 8160
Db 8101 ATATCATTTAATTTTAAATTCATAGTTTAAACATAATTTCTTAAATTAGTAGTTAAATA 8160
QY 8161 GAAGCAACCTCTCTTCCCTGCAGTGGCCTTCATTTAGTGAATATTTAGCTATTACATAG 8220
Db 8161 GAAGCAACCTCTCTTCCCTGCAGTGGCCTTCATTTAGTGAATATTTAGCTATTACATAG 8220
QY 8221 ACATATACCTTGGTAAAATTCATCTTCTTTCTAAATATACATAGTCAGATTAATATAT 8280
Db 8221 ACATATACCTTGGTAAAATTCATCTTCTTTCTAAATATACATAGTCAGATTAATATAT 8280
QY 8281 ATTTACTTTATGTTTCTTAGATCCCGGTAGCCTTTATTTTGTATTTTCTCCATTTTCTCT 8340
Db 8281 ATTTACTTTATGTTTCTTAGATCCCGGTAGCCTTTATTTTGTATTTTCTCCATTTTCTCT 8340
QY 8341 TTTAGATTTCTAAACTTGGTCATGGCACCATTAACAAATTTCTATAGCATTTTACAGTTTTT 8400
Db 8341 TTTAGATTTCTAAACTTGGTCATGGCACCATTAACAAATTTCTATAGCATTTTACAGTTTTT 8400
QY 8401 GAATAAATTTGCACAGGCACATATTTTCTTTTCTTTTACCCTCAGACAAATCTTTCACA 8460
Db 8401 GAATAAATTTGCACAGGCACATATTTTCTTTTCTTTTACCCTCAGACAAATCTTTCACA 8460
QY 8461 TGGTGGAAAAGGTATCATTTATGCCACCTTTTACTGAGATTTCTAAAGGAGGATTAAGTACC 8520
Db 8461 TGGTGGAAAAGGTATCATTTATGCCACCTTTTACTGAGATTTCTAAAGGAGGATTAAGTACC 8520
QY 8521 TTGTCAGAGGTCCTCCCTGACCTTGGACCTGGGACGAGGACCTGGGATCAGACATTTAA 8580
Db 8521 TTGTCAGAGGTCCTCCCTGACCTTGGACCTGGGACGAGGACCTGGGATCAGACATTTAA 8580
QY 8581 GCTCCTACATATTTCTGACTTTGAGGCTCTCTAACATGCTTCAATTTCTTTTATGTCT 8640
Db 8581 GCTCCTACATATTTCTGACTTTGAGGCTCTCTAACATGCTTCAATTTCTTTTATGTCT 8640
QY 8641 CAAGGCTGTCTGGCTCCCATGTGAACCCGCGAGGAGACCTGTGATGCTTTGCTGAA 8700
Db 8641 CAAGGCTGTCTGGCTCCCATGTGAACCCGCGAGGAGACCTGTGATGCTTTGCTGAA 8700
QY 8701 CTTTTGCTTAGGTGAAGTTAGATGCTGAGTCCCTGACCTATGCATCATGCATCAGGTCG 8760
Db 8701 CTTTTGCTTAGGTGAAGTTAGATGCTGAGTCCCTGACCTATGCATCATGCATCAGGTCG 8760
QY 8761 CACATTCCTTTTATTTAGAAATTTTGGCATGCTTCCATAGACGGTCCAGTGAGGACGG 8820
Db 8761 CACATTCCTTTTATTTAGAAATTTTGGCATGCTTCCATAGACGGTCCAGTGAGGACGG 8820
QY 8821 AATAAATCAGTGCATTTGTTTAAATGTTCAATCAAGTTAGGACCTCTCTGATGCAGAT 8880
Db 8821 AATAAATCAGTGCATTTGTTTAAATGTTCAATCAAGTTAGGACCTCTCTGATGCAGAT 8880
QY 8881 GGAAGATGGAGATCTGTTTGTAGAAAACCTTCAAAAGACTTGTGATGACAGATTTGGCAG 8940
Db 8881 GGAAGATGGAGATCTGTTTGTAGAAAACCTTCAAAAGACTTGTGATGACAGATTTGGCAG 8940
QY 8941 GGGTGGAGGAGGAATACCTTAAGTAAGTTCTTTAGGAGACAAAGTGTGACAGAAATTTT 9000
Db 8941 GGGTGGAGGAGGAATACCTTAAGTAAGTTCTTTAGGAGACAAAGTGTGACAGAAATTTT 9000

Db	11161	TTAAATGATTTTGACAGCCTTTAGAGGATATTGACTACATGTTGAGCCTACCAATGCT	11220
QY	11221	AGAAAACATTAATGAAAGCCTGGTGGGCACTACATTTACAGACATGGCATTAGCATGG	11280
Db	11221	AGAAAACATTAATGAAAGCCTGGTGGGCACTACATTTACAGACATGGCATTAGCATGG	11280
QY	11281	GTATCACTCATGACAGATGGGCCCTGCTGCTGGGAGTACCTTTGCCCCATGTGGCA	11340
Db	11281	GTATCACTCATGACAGATGGGCCCTGCTGCTGGGAGTACCTTTGCCCCATGTGGCA	11340
QY	11341	AGTTTGGCCTTTGGCAGGAGCCTGATGTGAAGCTAGATTGAGAAGGAGAGGTGTG	11400
Db	11341	AGTTTGGCCTTTGGCAGGAGCCTGATGTGAAGCTAGATTGAGAAGGAGAGGTGTG	11400
QY	11401	CAGTTTGTATACCTTAAACAAGAGTTCATACTTGTAACTGAGTCACTCAGGGAAGAA	11460
Db	11401	CAGTTTGTATACCTTAAACAAGAGTTCATACTTGTAACTGAGTCACTCAGGGAAGAA	11460
QY	11461	TGTAATCAGAACTGAGAAAGCCAGACGAGCTCTCATCTAATTTCCACCCACATCTGCTT	11520
Db	11461	TGTAATCAGAACTGAGAAAGCCAGACGAGCTCTCATCTAATTTCCACCCACATCTGCTT	11520
QY	11521	GTACTTTATAGTCTTCAGATGCCCTTATTCACCCAGTATCCCCAGGTGGTAAGAAGACA	11580
Db	11521	GTACTTTATAGTCTTCAGATGCCCTTATTCACCCAGTATCCCCAGGTGGTAAGAAGACA	11580
QY	11581	TGTGTATCATTTGCCATTTGTCAAGATGAGTGAATTAACTTTTTATAAGCAGTCTATAA	11640
Db	11581	TGTGTATCATTTGCCATTTGTCAAGATGAGTGAATTAACTTTTTATAAGCAGTCTATAA	11640
QY	11641	CATTTACTGPTCTGATCATATCTTTATTTTTCATTTTACCTAGCATTTTCAACCCACC	11700
Db	11641	CATTTACTGPTCTGATCATATCTTTATTTTTCATTTTACCTAGCATTTTCAACCCACC	11700
QY	11701	AATTTGTTTTTATCTTACACAAATTCATTAGATTTTGGGGCAGGATTAAGTGTAC	11760
Db	11701	AATTTGTTTTTATCTTACACAAATTCATTAGATTTTGGGGCAGGATTAAGTGTAC	11760
QY	11761	AACAGATATGAATATGATTAATTTTCAGGTTTGCCTGGGAACCTCAAAATTTGAGGTAT	11820
Db	11761	AACAGATATGAATATGATTAATTTTCAGGTTTGCCTGGGAACCTCAAAATTTGAGGTAT	11820
QY	11821	TATGGGATTAAGTAGGAAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGGTCCACGT	11880
Db	11821	TATGGGATTAAGTAGGAAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGGTCCACGT	11880
QY	11881	TGCCCCCTCCATGTGGCAAGCTGGAACCCAGACCCACATCTTTTCTAGTCCCTCAAGTTT	11940
Db	11881	TGCCCCCTCCATGTGGCAAGCTGGAACCCAGACCCACATCTTTTCTAGTCCCTCAAGTTT	11940
QY	11941	TCCTGCTCTATTTGCCCTCTCTTGGTAGGAAACATCACAGACCATGAGGCTTCACTTAAAG	12000
Db	11941	TCCTGCTCTATTTGCCCTCTCTTGGTAGGAAACATCACAGACCATGAGGCTTCACTTAAAG	12000
QY	12001	GTGGAGAAAGGACAAGAGGACAGACTCCACAAGTTCTAGCTATGAGTTTCCAAAAA	12060
Db	12001	GTGGAGAAAGGACAAGAGGACAGACTCCACAAGTTCTAGCTATGAGTTTCCAAAAA	12060
QY	12061	AATAACAGAAAGAGATTTCTTGACTTTTATTTATGTTAGGTATTAATCATGACCCAAA	12120
Db	12061	AATAACAGAAAGAGATTTCTTGACTTTTATTTATGTTAGGTATTAATCATGACCCAAA	12120
QY	12121	ACFCCCTCCCTATTTGCTAGAGAGGAAACTCTCTGGCGAAATTTATTTCTGTTTCTT	12180
Db	12121	ACFCCCTCCCTATTTGCTAGAGAGGAAACTCTCTGGCGAAATTTATTTCTGTTTCTT	12180
QY	12181	TGCTCTCAATTTGAAATTTAGGTACTTTTTTTTCAATAACAGACGTTTCAACATGTAA	12240
Db	12181	TGCTCTCAATTTGAAATTTAGGTACTTTTTTTTCAATAACAGACGTTTCAACATGTAA	12240
QY	12241	AAACAAGTACTATTTCTTTTACCTCAAAATCTGAAGTCAACAGTGTATTACTTACCTC	12300
Db	12241	AAACAAGTACTATTTCTTTTACCTCAAAATCTGAAGTCAACAGTGTATTACTTACCTC	12300

QY	12301	ATATTTCACTGATAAAATACAGATGCTCGTTGACTTATGATGGGCTATATCTCTGATAAAC	12360
Db	12301	ATATTTCACTGATAAAATACAGATGCTCGTTGACTTATGATGGGCTATATCTCTGATAAAC	12360
QY	12361	CCATTTGAGGTTTAAAAATATTTTAAAGTTGAAAAATGCAATTAATACCCCCCAATACCCAC	12420
Db	12361	CCATTTGAGGTTTAAAAATATTTTAAAGTTGAAAAATGCAATTAATACCCCCCAATACCCAC	12420
QY	12421	TGAAAAAGTAAAAAAGAAAAAATCTAAATCTAACCATCATTTGAGGATAATCTGTACCAAT	12480
Db	12421	TGAAAAAGTAAAAAAGAAAAAATCTAAATCTAACCATCATTTGAGGATAATCTGTACCAAT	12480
QY	12481	TTATTAATACATCTCCTAATCTTAAACTGTGATAAAATGCAATGTTTAAATACAAATTT	12540
Db	12481	TTATTAATACATCTCCTAATCTTAAACTGTGATAAAATGCAATGTTTAAATACAAATTT	12540
QY	12541	CTACCTTAGAACAAAGAAAGTCAATTTTTTTTCAATTTTCTGTAGATGTCTAGTGTATTC	12600
Db	12541	CTACCTTAGAACAAAGAAAGTCAATTTTTTTTCAATTTTCTGTAGATGTCTAGTGTATTC	12600
QY	12601	TAGATGCTATAAATGTGCCAGAAATCAGATAGGTATAGGCTTGTGCCATTCACAAAGGT	12660
Db	12601	TAGATGCTATAAATGTGCCAGAAATCAGATAGGTATAGGCTTGTGCCATTCACAAAGGT	12660
QY	12661	AGTCAGGGCCTTCTGTTGTTAAATTTCAATTTAGTTAAAACTAAATAAAAATTAATAA	12720
Db	12661	AGTCAGGGCCTTCTGTTGTTAAATTTCAATTTAGTTAAAACTAAATAAAAATTAATAA	12720
QY	12721	TTTAGTTTCTATTTGTCTACACATTTCAAGTGGCCCAACGCCACATGTTGCTAGTGA	12780
Db	12721	TTTAGTTTCTATTTGTCTACACATTTCAAGTGGCCCAACGCCACATGTTGCTAGTGA	12780
QY	12781	CTACCATATGGAACATTTGCAAAATATAGTTTATCTATCTACACAGGAGATCTATTAGA	12840
Db	12781	CTACCATATGGAACATTTGCAAAATATAGTTTATCTATCTACACAGGAGATCTATTAGA	12840
QY	12841	CAGTCAGGTGGTGTAGTCAAGCATCTCAGAAAAATTTATGAGAGGAGAACACAGGAAAT	12900
Db	12841	CAGTCAGGTGGTGTAGTCAAGCATCTCAGAAAAATTTATGAGAGGAGAACACAGGAAAT	12900
QY	12901	TAACATCTATCTTTTATCTCTTTGATGCTTCTCTATGTTTGGCTGTTGACTTAATGATA	12960
Db	12901	TAACATCTATCTTTTATCTCTTTGATGCTTCTCTATGTTTGGCTGTTGACTTAATGATA	12960
QY	12961	CAGCAGGCGCACCACAAATCATGAAAAACAGTTGAGTAATAATTTAAATAGTCTACTATCTT	13020
Db	12961	CAGCAGGCGCACCACAAATCATGAAAAACAGTTGAGTAATAATTTAAATAGTCTACTATCTT	13020
QY	13021	TTAGGAAATATCTCTTCTCTTCAATATACACTATCAAGAGAGAACCTGAAATTAATAGT	13080
Db	13021	TTAGGAAATATCTCTTCTCTTCAATATACACTATCAAGAGAGAACCTGAAATTAATAGT	13080
QY	13081	TTCTTCTAATTTGCTACAAATACGTTTCTGGAATCTCTCCCTTTAAACAAAAATCACTA	13140
Db	13081	TTCTTCTAATTTGCTACAAATACGTTTCTGGAATCTCTCCCTTTAAACAAAAATCACTA	13140
QY	13141	CCCAATTTATCTTTTATCTATGATGGGTTTCTGAGGACTGTACTCTCCCAATGTTTTA	13200
Db	13141	CCCAATTTATCTTTTATCTATGATGGGTTTCTGAGGACTGTACTCTCCCAATGTTTTA	13200
QY	13201	AGCTGAAGGAATTTGAGAAAAACAGAAAAAGACAGAAAGATCACCTCTGACCTTCCCTCACC	13260
Db	13201	AGCTGAAGGAATTTGAGAAAAACAGAAAAAGACAGAAAGATCACCTCTGACCTTCCCTCACC	13260
QY	13261	CTCCATCTGAAGAGTCAATAAACCTAGGATTTTCTGACCTTCCCATGTAGCAAGTCA	13320
Db	13261	CTCCATCTGAAGAGTCAATAAACCTAGGATTTTCTGACCTTCCCATGTAGCAAGTCA	13320
QY	13321	TAGACCCCTCATCGGAGAGGTGCCCTGTTTATACCCAGAGAAAGAAATTTCCCCCCCG	13380
Db	13321	TAGACCCCTCATCGGAGAGGTGCCCTGTTTATACCCAGAGAAAGAAATTTCCCCCCCG	13380

QY	13381	CTTTTGTGTTGAGATGTTGCTTACTCTGTCAACCAGGCTAGAGTGCAGTTGCTATGATC	13440		Db	14461	ACTAGGCTCAAGCAACCCCACTTCTGGAAATGGAATAAGACCTTTTGTCTGTTTCCACAG	14520	
Db	13381	CTTTTGTGTTGAGATGTTGCTTACTCTGTCAACCAGGCTAGAGTGCAGTTGCTATGATC	13440		QY	14521	GGCACTTGACAGTGAATTTGTGCACATCTCAAGGTTATTTTCAGGAGTCTCAGGGGCAT	14580	
QY	13441	ATGTTCTGTCGAACCTTGAACCTCTGGCTCAAGCAATTCCTGCTCAGCTCCCAA	13500		Db	14521	GGCACTTGACAGTGAATTTGTGCACATCTCAAGGTTATTTTCAGGAGTCTCAGGGGCAT	14580	
Db	13441	ATGTTCTGTCGAACCTTGAACCTCTGGCTCAAGCAATTCCTGCTCAGCTCCCAA	13500		QY	14581	ATGACAGGAGTGTGTTCCAGGTAAAGCACTTACTGGCTGGTGATGATGTTATTTTC	14640	
QY	13501	GTAGCTCAGACACAGACACATCTCCACATTTGGCTACTTAAATAATTCCTTTTTT	13560		Db	14581	ATGACAGGAGTGTGTTCCAGGTAAAGCACTTACTGGCTGGTGATGATGTTATTTTC	14640	
Db	13501	GTAGCTCAGACACAGACACATCTCCACATTTGGCTACTTAAATAATTCCTTTTTT	13560		QY	14641	CTTTCACTCAGACATTTGACAGAGTGAATTTATAGAGCTTTTGAGAGTCTTAGAAGTAA	14700	
QY	13561	TATTAATTAATTTATTTTATAGAGATGGGGGCTCTCGCTATGTTGACCCGGTTGAT	13620		Db	14641	CTTTCACTCAGACATTTGACAGAGTGAATTTATAGAGCTTTTGAGAGTCTTAGAAGTAA	14700	
Db	13561	TATTAATTAATTTATTTTATAGAGATGGGGGCTCTCGCTATGTTGACCCGGTTGAT	13620		QY	14701	ATATTAGGACACATGCTTTAAAGAGATGCTTTAGATACAGTCTTCAAGGATGCCAATGTT	14760	
QY	13621	CTTGAACCTATAGCCTCAAGGATCATCCACCTTGGCTCTCAAGTGTCTGAGATTACA	13680		Db	14701	ATATTAGGACACATGCTTTAAAGAGATGCTTTAGATACAGTCTTCAAGGATGCCAATGTT	14760	
Db	13621	CTTGAACCTATAGCCTCAAGGATCATCCACCTTGGCTCTCAAGTGTCTGAGATTACA	13680		QY	14761	TCAAATCCACTCATGCGACTGAACAAAGAGATCAAGAGTTCCTCCCTCTACACATTAAC	14820	
QY	13681	GGCATGAGCCACTGCTCCTGGCTAAGAAATCCTTATCTCAAGACAAAGGTAGAACAA	13740		Db	14761	TCAAATCCACTCATGCGACTGAACAAAGAGATCAAGAGTTCCTCCCTCTACACATTAAC	14820	
Db	13681	GGCATGAGCCACTGCTCCTGGCTAAGAAATCCTTATCTCAAGACAAAGGTAGAACAA	13740		QY	14821	GAGAACAGAAATTTGCAAGTAATGTTTATGTTAGAGAGATAAGAAAGAACTAAGAGG	14880	
QY	13741	TAGAATCTGAACAAACAGCCCTTGCTAATTTTCCAGTGTATTAACATTAAGATCATAC	13800		Db	14821	GAGAACAGAAATTTGCAAGTAATGTTTATGTTAGAGAGATAAGAAAGAACTAAGAGG	14880	
Db	13741	TAGAATCTGAACAAACAGCCCTTGCTAATTTTCCAGTGTATTAACATTAAGATCATAC	13800		QY	14881	AGGAGGTAGCCAGGCTTCAGTGTCTTCAAACTTAAGTAAATTTTAAATCAAGCTAAA	15000	
QY	13801	TCGCGCTATCATATTTCTCCACACTATCCACACTTTATCAAACTTACTGTAAAAAAT	13860		Db	14881	AGGAGGTAGCCAGGCTTCAGTGTCTTCAAACTTAAGTAAATTTTAAATCAAGCTAAA	15000	
Db	13801	TCGCGCTATCATATTTCTCCACACTATCCACACTTTATCAAACTTACTGTAAAAAAT	13860		QY	14941	TGGGGTCTATGTTTCACTCTCTCCCACTAAAGTAAATTTTAAATCAAGCTAAA	15000	
QY	13861	ATCAGGTTGAACACACTTTTGGGCTCTCTTACCAAGGCTCTGTGTCAAGTAAACAT	13920		Db	14941	TGGGGTCTATGTTTCACTCTCTCCCACTAAAGTAAATTTTAAATCAAGCTAAA	15000	
Db	13861	ATCAGGTTGAACACACTTTTGGGCTCTCTTACCAAGGCTCTGTGTCAAGTAAACAT	13920		QY	15001	AATTTCTATCTAGCATAGAGTCAAGATAAAATAAAGCACTCCCAAAATACATCAAGTC	15060	
QY	13921	ATTCATAAATGAGTACACTTTTCCCTTGTATTCGTCTTTTGTATAGTGGCCTCAGC	13980		Db	15001	AATTTCTATCTAGCATAGAGTCAAGATAAAATAAAGCACTCCCAAAATACATCAAGTC	15060	
Db	13921	ATTCATAAATGAGTACACTTTTCCCTTGTATTCGTCTTTTGTATAGTGGCCTCAGC	13980		QY	15061	CTGACCTTGAATGTTCTTCCCTCAGAGTACTACTAGGTAGAGACCTTGTCTCTCTAGA	15120	
QY	13981	CATGAACCTTAGAAGGTTGGAAGAAAGGTATTTTCCCTACTATATCTAGTATATTC	14040		Db	15061	CTGACCTTGAATGTTCTTCCCTCAGAGTACTACTAGGTAGAGACCTTGTCTCTCTAGA	15120	
Db	13981	CATGAACCTTAGAAGGTTGGAAGAAAGGTATTTTCCCTACTATATCTAGTATATTC	14040		QY	15121	TTATTTTAACTATAACCTGATTACTGCAATTCGCAATTTATCTTGGGTATGATTAAAGG	15180	
QY	14041	AAGAAGCATAGATGATTTTGAAGAGAGGAAATACTTCAACAGGCTACTTCAAAAC	14100		Db	15121	TTATTTTAACTATAACCTGATTGCAATTCGCAATTTATCTTGGGTATGATTAAAGG	15180	
Db	14041	AAGAAGCATAGATGATTTTGAAGAGAGGAAATACTTCAACAGGCTACTTCAAAAC	14100		QY	15181	TTATAAAATTCAGGTTCTTAGAAGTGAAGGCAACATCCCAATCTAGAGTTCATCAGTTCA	15240	
QY	14101	TTTTGAGCAAGAAATAAAGACAGTCAATTTTACTGCACAGTGAACCCGCTCAA	14160		Db	15181	TTATAAAATTCAGGTTCTTAGAAGTGAAGGCAACATCCCAATCTAGAGTTCATCAGTTCA	15240	
Db	14101	TTTTGAGCAAGAAATAAAGACAGTCAATTTTACTGCACAGTGAACCCGCTCAA	14160		QY	15241	TACAAATAAACAACATGAACATAGATGATGATGATGATGATGATGATGATGATGATGATG	15300	
QY	14161	AACTTACAGGACAACTAATATGACCTGTGAAGAAAGCAATATTAGCTTCGTTAGAAGT	14220		Db	15241	TACAAATAAACAACATGAACATAGATGATGATGATGATGATGATGATGATGATGATGATG	15300	
Db	14161	AACTTACAGGACAACTAATATGACCTGTGAAGAAAGCAATATTAGCTTCGTTAGAAGT	14220		QY	15301	TTTCTCTTGAACAGTGGGTGGATCAAGCAATTTCTTATGACTTAAAGAAAATATGTTCC	15360	
QY	14221	TTCCAGTTTCCAGATTTAAATTCCTTAAGGTTGAGCACTGAAATATTTGTTGGAGATCA	14280		Db	15301	TTTCTCTTGAACAGTGGGTGGATCAAGCAATTTCTTATGACTTAAAGAAAATATGTTCC	15360	
Db	14221	TTCCAGTTTCCAGATTTAAATTCCTTAAGGTTGAGCACTGAAATATTTGTTGGAGATCA	14280		QY	15361	ATGTAGGGCTAAAATAGTGTTCCTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	15420	
QY	14281	CACAGCCCTGTTATGTGACAAGGCTCTATTAACCCCTTAAAGGCTGCTATCTTTCACAGA	14340		Db	15361	ATGTAGGGCTAAAATAGTGTTCCTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	15420	
Db	14281	CACAGCCCTGTTATGTGACAAGGCTCTATTAACCCCTTAAAGGCTGCTATCTTTCACAGA	14340		QY	15421	CCTACATTTTCCCAAGTGAAGATATCAATTTATACATCTCAATTTTGGTCTTAATCCAGAA	15480	
QY	14341	AACTCATTTTCACATCTCATCAGTTGCAACCATGAGCTGGGAAACTGGTTCTCATTTCT	14400		Db	15421	CCTACATTTTCCCAAGTGAAGATATCAATTTATACATCTCAATTTTGGTCTTAATCCAGAA	15480	
Db	14341	AACTCATTTTCACATCTCATCAGTTGCAACCATGAGCTGGGAAACTGGTTCTCATTTCT	14400		QY	15481	GTTACTCTCTACTTACTACGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	15540	
QY	14401	CAGAGTGAAGATACAGACACAGAAATTCAGAAATAAAGGACTAGAAATTTTCCCTTAATGAG	14460		Db	15481	GTTACTCTCTACTTACTACGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	15540	
Db	14401	CAGAGTGAAGATACAGACACAGAAATTCAGAAATAAAGGACTAGAAATTTTCCCTTAATGAG	14460		QY	15541	CACCACCACCACCAAGGCTCCAAAACAGTTTACAAAGCTGGAGATTTTGTGTTTGTGTTT	15600	
QY	14461	ACTAGGCTCAAGCAACCCCACTTCTGGAAATGGAATAAGCCCTTTTGTGTTTCCACAG	14520						

Db	15541	CACCACCAACACACAAAGCCCTCCAAACAAACAGTTTAAACAGCTGGAGATTTGCTTTA	15600
QY	15601	GAGAGAACTACCTATTTCCCTTGTGTGGTGACACCTTTTAAACAAATATATATATATCTTT	15660
Db	15601	GAGAGAACTACCTATTTCCCTTGTGTGGTGACACCTTTTAAACAAATATATATATATCTTT	15660
QY	15661	AAGTTGTGGGATACTTGTGCAGAACGTGCAGGTTTCTAGTAGGTATACACGTGCCATG	15720
Db	15661	AAGTTGTGGGATACTTGTGCAGAACGTGCAGGTTTCTAGTAGGTATACACGTGCCATG	15720
QY	15721	GTGGTTGTGTCACCCCTTTAAACCCATCACTACATTTAGTATTTCTCCTAAAGCTATGCC	15780
Db	15721	GTGGTTGTGTCACCCCTTTAAACCCATCACTACATTTAGTATTTCTCCTAAAGCTATGCC	15780
QY	15781	TCCCCAAACCCCAACCCAGCAGCCCGCTGATGTGATGTTCCCTTCCCTGTGTC	15840
Db	15781	TCCCCAAACCCCAACCCAGCAGCCCGCTGATGTGATGTTCCCTTCCCTGTGTC	15840
QY	15841	TGTGTTCACTCTCACTTATGAGTGAGAACATGTGTGTGGTTGTTTCTGCTGTGTT	15900
Db	15841	TGTGTTCACTCTCACTTATGAGTGAGAACATGTGTGTGGTTGTTTCTGCTGTGTT	15900
QY	15901	AGTTTCTGAGATGATGTTTCTAGCTTCATCCGCTCTCTGCAAGGACGTGAACCTCA	15960
Db	15901	AGTTTCTGAGATGATGTTTCTAGCTTCATCCGCTCTCTGCAAGGACGTGAACCTCA	15960
QY	15961	TCCTTTTAAAGGCTCAAGATTTCCATGGTGTATGTGTCACATTTCTTATCCAG	16020
Db	15961	TCCTTTTAAAGGCTCAAGATTTCCATGGTGTATGTGTCACATTTCTTATCCAG	16020
QY	16021	TCATCACTGATGGGATTTGGTGTGTTCCAGTCTTTGCTATTTGTGAATAGTGTGCA	16080
Db	16021	TCATCACTGATGGGATTTGGTGTGTTCCAGTCTTTGCTATTTGTGAATAGTGTGCA	16080
QY	16081	ATAACATATGTGTCATGCTCTTATAGCAGAACTATTAATCAATTTGCTATATAC	16140
Db	16081	ATAACATATGTGTCATGCTCTTATAGCAGAACTATTAATCAATTTGCTATATAC	16140
QY	16141	CCAGTAATGGGATTTGCTGGACACTGATGGAGAGCACTCAACAGTAACTTCTTAACAA	16200
Db	16141	CCAGTAATGGGATTTGCTGGACACTGATGGAGAGCACTCAACAGTAACTTCTTAACAA	16200
QY	16201	TGATGTTGCTCATATTTAGTTTATATTTTAAACATATTTCTGCATGATGTTTAAACA	16260
Db	16201	TGATGTTGCTCATATTTAGTTTATATTTTAAACATATTTCTGCATGATGTTTAAACA	16260
QY	16261	TCTTGCAAAATATATTTTATATGATGATTTTATTTTACCTCAGAGCACTCTGGAAG	16320
Db	16261	TCTTGCAAAATATATTTTATATGATGATTTTATTTTACCTCAGAGCACTCTGGAAG	16320
QY	16321	GGTTATCTGATATATTTTTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	16380
Db	16321	GGTTATCTGATATATTTTTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	16380
QY	16381	TGATGACTTGATGTTTCCACAATATTAAGTAAATTTAGAGCTGCTGCTGATGTCAG	16440
Db	16381	TGATGACTTGATGTTTCCACAATATTAAGTAAATTTAGAGCTGCTGCTGATGTCAG	16440
QY	16441	GAAGAGCTCTAAGCT	16500
Db	16441	GAAGAGCTCTAAGCT	16500
QY	16501	TGTATATATATATATATATACACACACACACACACATATATATATATATATATA	16560
Db	16501	TGTATATATATATATATATACACACACACACACACACATATATATATATATATA	16560
QY	16561	TGTAATTTTGTGAGATGAGTTTCTTTTACCCAGGCTGGAGTGCATGCGCGATC	16620
Db	16561	TGTAATTTTGTGAGATGAGTTTCTTTTACCCAGGCTGGAGTGCATGCGCGATC	16620
QY	16621	TCAGCTCACTGCAACCTCCGCTCTCCGGTTCAAGTATCTCCGCTCAGCTCCTGA	16680
Db	16621	TCAGCTCACTGCAACCTCCGCTCTCCGGTTCAAGTATCTCCGCTCAGCTCCTGA	16680
QY	16681	GTAGCTGGGATACAGGTGCCATCAGCCTGGCTAATTTTGTATTTTGTATTTAGTAGAG	16740
Db	16681	GTAGCTGGGATACAGGTGCCATCAGCCTGGCTAATTTTGTATTTTGTATTTAGTAGAG	16740
QY	16741	ACGGGTTTGGCATGTTGGCCACGCTGTTTGAACCTCCTGACCTCAGGTGATCACC	16800
Db	16741	ACGGGTTTGGCATGTTGGCCACGCTGTTTGAACCTCCTGACCTCAGGTGATCACC	16800
QY	16801	ACCTCCGCTCCCAAAAGTCTAGGATACAGGCTGAGCCTGCGCCGCTATCTTT	16860
Db	16801	ACCTCCGCTCCCAAAAGTCTAGGATACAGGCTGAGCCTGCGCCGCTATCTTT	16860
QY	16861	TATGCTCAATAAAGTCTATATATTTACTAGTGTATAAGAAACCATAGACCCTGGAACCA	16920
Db	16861	TATGCTCAATAAAGTCTATATATTTACTAGTGTATAAGAAACCATAGACCCTGGAACCA	16920
QY	16921	GTGGATTTGAGTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16980
Db	16921	GTGGATTTGAGTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16980
QY	16981	ACTGATCTCTTAGGCTCAGTTTACTCACCTATAAAAGAAATATAAATAGTGACATT	17040
Db	16981	ACTGATCTCTTAGGCTCAGTTTACTCACCTATAAAAGAAATATAAATAGTGACATT	17040
QY	17041	TTTACAATATTTGTTGATGGGCTGCTAAATGAGCTAATGATTACTTACAATAGTTTGTGTC	17100
Db	17041	TTTACAATATTTGTTGATGGGCTGCTAAATGAGCTAATGATTACTTACAATAGTTTGTGTC	17100
QY	17101	AAGCAATAAATGCTGTTTACTTATTTAAAGTTTATGCTCTTAAAGTTTGTGTC	17160
Db	17101	AAGCAATAAATGCTGTTTACTTATTTAAAGTTTATGCTCTTAAAGTTTGTGTC	17160
QY	17161	TCCTATATCTTTTACTTTTGTCTATTTTGTGCAATATCCAGAGCTGATTCCTGAGTAG	17220
Db	17161	TCCTATATCTTTTACTTTTGTCTATTTTGTGCAATATCCAGAGCTGATTCCTGAGTAG	17220
QY	17221	CACCTAATAATAGTTAAATGAGCACTTTCCGCTGTTGAAACATCTTCATATTTAGA	17280
Db	17221	CACCTAATAATAGTTAAATGAGCACTTTCCGCTGTTGAAACATCTTCATATTTAGA	17280
QY	17281	AAATAAAGATCTTTGACAAATTTATTTTGTCTATCTTTTGTGCTGCTGCTGCTGCTGCT	17340
Db	17281	AAATAAAGATCTTTGACAAATTTATTTTGTCTATCTTTTGTGCTGCTGCTGCTGCTGCT	17340
QY	17341	TGATATAATTAAGTTTAAAGTTTATGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17400
Db	17341	TGATATAATTAAGTTTAAAGTTTATGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17400
QY	17401	AACATCATATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	17460
Db	17401	AACATCATATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	17460
QY	17461	TATCATATTTTCAATATATATTTCAATATTTGATTTGATTTGATTTGATTTGATTTGATTTG	17520
Db	17461	TATCATATTTTCAATATATATTTCAATATTTGATTTGATTTGATTTGATTTGATTTGATTTG	17520
QY	17521	CAAAATAGAAAAAAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17580
Db	17521	CAAAATAGAAAAAAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17580
QY	17581	CTTGGCAAAACCTAGTGGGTAGAAATTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	17640
Db	17581	CTTGGCAAAACCTAGTGGGTAGAAATTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	17640
QY	17641	TGTGCTGATGAAACCTGAACTGTAATGCAATGCCCCCTGCTTCTTCTTCTTCTTCTTCTT	17700
Db	17641	TGTGCTGATGAAACCTGAACTGTAATGCAATGCCCCCTGCTTCTTCTTCTTCTTCTTCTT	17700
QY	17701	TTAAGCATTTCAACAAAGAAATCTAAGAATGACATCTCTGATGATCTTTTCTACGGTTT	17760
Db	17701	TTAAGCATTTCAACAAAGAAATCTAAGAATGACATCTCTGATGATCTTTTCTACGGTTT	17760

QY	17761	CCCTGAATGGATGTCAGGACCTCCAGTTGACAGTTCCACAGCCACAAATTTCCCTCCACA	17820
Db	17761		
QY	17821	GGCTGACGAGGAGGACGTCGGAAGAGACACACATTTGGCAACTTCAGCTCTCTCT	17880
Db	17821		
QY	17881	TATATTGACCGAGTAATTCCTGGGAGTGAACCTGTAACGCTTGGCATCATCATTCAGGCT	17940
Db	17881		
QY	17941	ATCCAGGTCAACTGTAAGCAAAATACATGCACCTGTGTAAGCAAAACACACAGTAAGCACAA	18000
Db	17941		
QY	18001	TTGCTCAGCATGTGTTTGGGGAATAGAGTGGGAAGATTCGTGAGGACAACTTTAATCC	18060
Db	18001		
QY	18061	TGGGATTAATCCATCTCAGGCTCTCAATTAATCTGGGAACCTFAAAGTAAAGACCTAAT	18120
Db	18061		
QY	18121	TCTCTTTGATCCCATCTACCCCTTTGAAAATAACAAACAAAACAAAACAAAAC	18180
Db	18121		
QY	18181	TTGGCTAAATTCATGTCTGGTTCAAATTTCCCTTGGCATCTTTTATGCAAAAAGTT	18240
Db	18181		
QY	18241	CAGAGAAAGAAATGAACATTTGGCAAAATTAATAATTAATTCCTTTATGCAAAAAGTT	18300
Db	18241		
QY	18301	CAAAATAAAGTCTCTTCAATCTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	18360
Db	18301		
QY	18361	ATTTAAATATATCTAGGACACATTAAGACAAACACCTGTATATATTTACCTGCGACGT	18420
Db	18361		
QY	18421	AAATTTACACATAAATGTAATAAGAAAGGTTTTAGTTTTATTTTAACTTCAAAAGT	18480
Db	18421		
QY	18481	TAATCAACATGTTAGAGAAATGATTTTTTTGTGTGTAATGATGTCATATTTGTGCAC	18540
Db	18481		
QY	18541	TGGGTCTAGATGGCAGTATAGCATAGTGGTTAAGTCTTTGGAGCCGACGTAAGTTAC	18600
Db	18541		
QY	18601	AACCTGCCATCATCATGAGTATCTTTCCCTTTTGTGTTAGTTGGAAGTTATTTAATGGCT	18660
Db	18601		
QY	18661	CTGAACCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18720
Db	18661		
QY	18721	CTGACTCAATGCGGAGTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18780
Db	18721		
QY	18781	TTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18840
Db	18781		
QY	18841	TTATGTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18900
Db	18841		

Db	18841		
QY	18901	TCTATGAATCAAAAGCACCAATATTTTCAAGCTAAGTCTAATAATTTACTTTGAAT	18960
Db	18901		
QY	18961	CAATTCGATTAATTCGTTTACATAAATAGATTTGATTTCTGTTCTTCAAGTCCATCCA	19020
Db	18961		
QY	19021	ATTATCCATCAATTTGGCAGCCAAATCCTCTTATTGTTGTCATACATAGTATCTTC	19080
Db	19021		
QY	19081	TCACAAGAACACAGTTAGAACCAAGTCTTTTGTCTGCACAGAACCCACCCCTTCCC	19140
Db	19081		
QY	19141	AATGCACGCCCTTGTGTCACAGCCACACAGAGGAATCCCATGAATGTTAGGCAGT	19200
Db	19141		
QY	19201	TATCACCATGTTCTAATCTTAACTCTAGCCCTGGTAAATGTTCTTAGGCTTAACTGAACT	19260
Db	19201		
QY	19261	GCTTAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	19320
Db	19261		
QY	19321	TCAGTAGAATGCATCTAAGGAAATTTGAGGAAACAAAGTGTGACCATGAGTCCACTAAC	19380
Db	19321		
QY	19381	GCATCCCTGTTGCTTTTATATCTACAACTGTCTTTGATTTCTCAAGGCGAGGATTT	19440
Db	19381		
QY	19441	ATCCCAATTTGTCATACCTGTAGCCAGGATCTGTGGAACTTAATAATGCGCAAAATA	19500
Db	19441		
QY	19501	TCAGTGTGATAAATTTATTTGCTTTTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	19560
Db	19501		
QY	19561	GCTATAATCAATCCAGATTTAAATGAACTGTCTTTGGGAAAGGAAAGGATTTTAT	19620
Db	19561		
QY	19621	TGCTGTAAAGCCCTGAAATAAATCTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	19680
Db	19621		
QY	19681	AGAAAGTGAGCAATCATCCATTACAAGTGTCAACCTTGAGATAAATACTGCTGGCCTG	19740
Db	19681		
QY	19741	TGCATTTCTGGGCTTGTGAACAGGCTGATGAGAGGCCAAATCTGCTGTTGTGATAA	19800
Db	19741		
QY	19801	TGGGAAGATTTTCTTAACACGAGGAGTAAAGAGGTACAAATAGCAGGAGGATCGT	19860
Db	19801		
QY	19861	GATGTGTGAGAGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	19920
Db	19861		
QY	19921	TTGAGCCCTCTGCTGAACTATGTCATACCTTACAGATATGACTACATTTAGTTGTTCC	19980
Db	19921		

Db	19921	TTGAGCCCTCTGCTGAACATATGTCATAAACCTTACAGATATGACTACATATTTAGTTGTTC	19980
Qy	19981	CAOCCATTTCAAGTGAAGTATATTTGCTAAGAGTTAACAGTAAATGCTAAACTGGAAAT	20040
Db	19981	CAOCCATTTCAAGTGAAGTATATTTGCTAAGAGTTAACAGTAAATGCTAAACTGGAAAT	20040
Qy	20041	GAAGCCTTTCCOCCCTTTTGCTGCTCATAGTCTGTGCTCACTTTAAGCAGAATAAGAGGATG	20100
Db	20041	GAAGCCTTTCCOCCCTTTTGCTGCTCATAGTCTGTGCTCACTTTAAGCAGAATAAGAGGATG	20100
Qy	20101	CAGTAAGCCATAGTTGAAGGAAGAACAGCAGTGTATGAGGCTGTACTGGACTTTTCCT	20160
Db	20101	CAGTAAGCCATAGTTGAAGGAAGAACAGCAGTGTATGAGGCTGTACTGGACTTTTCCT	20160
Qy	20161	GTCTGATGTTGAACACGAGGTTGGGTGGTGAATGCCACATCTTATCTTCAGAGACACC	20220
Db	20161	GTCTGATGTTGAACACGAGGTTGGGTGGTGAATGCCACATCTTATCTTCAGAGACACC	20220
Qy	20221	CAAGCCAAAGTACAGCATGCTTCCCTATAGGAATTCCAATAACTCCAAAGTGCCCTCC	20280
Db	20221	CAAGCCAAAGTACAGCATGCTTCCCTATAGGAATTCCAATAACTCCAAAGTGCCCTCC	20280
Qy	20281	ACAAACAGAGAGGAGCATGTAAGCCCTCATCTTATTTGAACCAAACTCCTCAGATTGTA	20340
Db	20281	ACAAACAGAGAGGAGCATGTAAGCCCTCATCTTATTTGAACCAAACTCCTCAGATTGTA	20340
Qy	20341	TAACCTCTTTGACTAGCATTTGTTTACTTTTCTTACTCACCATGAGGAGATTCACAAT	20400
Db	20341	TAACCTCTTTGACTAGCATTTGTTTACTTTTCTTACTCACCATGAGGAGATTCACAAT	20400
Qy	20401	TCGTGCTAGTTTATGCAATCAATTCACATAATGCTCACTAAGAACTGTGACCCAGTGTACTG	20460
Db	20401	TCGTGCTAGTTTATGCAATCAATTCACATAATGCTCACTAAGAACTGTGACCCAGTGTACTG	20460
Qy	20461	CTGTAGAACTCACTGCTGCTACATATCAGCGGATGGAATCACCAGGAGCACTCAATTTAG	20520
Db	20461	CTGTAGAACTCACTGCTGCTACATATCAGCGGATGGAATCACCAGGAGCACTCAATTTAG	20520
Qy	20521	AAITAGAACTGAAAGTTGTTCTGACTGGATGCAAAATAACTTCAAAGCGTGAATGCAGAC	20580
Db	20521	AAITAGAACTGAAAGTTGTTCTGACTGGATGCAAAATAACTTCAAAGCGTGAATGCAGAC	20580
Qy	20581	TTTCTGAGGGATATTTAGTTTCTCAGTCAAGAAAGTCAATGAGCCAGTGCAGAGAGC	20640
Db	20581	TTTCTGAGGGATATTTAGTTTCTCAGTCAAGAAAGTCAATGAGCCAGTGCAGAGAGC	20640
Qy	20641	AGGAGCCAGACAGAGCTCAGCAGCAATTAAGGTTTCTGCTGCTGGGTTAGAAGGAGA	20700
Db	20641	AGGAGCCAGACAGAGCTCAGCAGCAATTAAGGTTTCTGCTGCTGGGTTAGAAGGAGA	20700
Qy	20701	ATTCTAGAGTGAAGTCTCTGGAGGAGACAGGCCAAGTGTGTCAACCCAGAGAGAGGG	20760
Db	20701	ATTCTAGAGTGAAGTCTCTGGAGGAGACAGGCCAAGTGTGTCAACCCAGAGAGAGGG	20760
Qy	20761	GCTGCCCTTTCTGTTCTGCTGATGCTCCTCATAGCTGAACATTCAGAGCATCAAGGGTGT	20820
Db	20761	GCTGCCCTTTCTGTTCTGCTGATGCTCCTCATAGCTGAACATTCAGAGCATCAAGGGTGT	20820
Qy	20821	TCCAAATTTAATTCAGAGGCCCTCAATTTCACTACGTCCTTATTTTCAATCCAGTCT	20880
Db	20821	TCCAAATTTAATTCAGAGGCCCTCAATTTCACTACGTCCTTATTTTCAATCCAGTCT	20880
Qy	20881	ACATCATGGAATAATCCCTTTTCTGCTCATTTGTAATTTAGTTTGTGCTTTATCAAG	20940
Db	20881	ACATCATGGAATAATCCCTTTTCTGCTCATTTGTAATTTAGTTTGTGCTTTATCAAG	20940
Qy	20941	CTCTTTGACATCAATTAAGTTTGTGGCCCTCATACAGGAGTTTCTTGGAAAGGCTGGG	21000
Db	20941	CTCTTTGACATCAATTAAGTTTGTGGCCCTCATACAGGAGTTTCTTGGAAAGGCTGGG	21000
Qy	21001	AAGGCTCCCTGCTCCTCAAAACTTCCTTTGGACATACACTGGTAAAGTGGGGTGTGCA	21060
Db	21001	AAGGCTCCCTGCTCCTCAAAACTTCCTTTGGACATACACTGGTAAAGTGGGGTGTGCA	21060
Qy	21061	CAGTGACAGGGCGCACATTTTCTCTGAGCCCTGCTCTAGGTGACGCTTAATCACA	21120
Db	21061	CAGTGACAGGGCGCACATTTTCTCTGAGCCCTGCTCTAGGTGACGCTTAATCACA	21120
Qy	21121	GAGGTGCTTTGAGATGTAATAAGATGCTGGGATCTGAGCTCTAGAAATGGGATGTGAAT	21180
Db	21121	GAGGTGCTTTGAGATGTAATAAGATGCTGGGATCTGAGCTCTAGAAATGGGATGTGAAT	21180
Qy	21181	GCACACCTTTTATAGTCTTCTTAATATTTAGGTGGGAGGAGAGTCAACCTGTTCCT	21240
Db	21181	GCACACCTTTTATAGTCTTCTTAATATTTAGGTGGGAGGAGAGTCAACCTGTTCCT	21240
Qy	21241	TTTGTATCTGCTGCTATAGTACTTAAAGTCTGTGTTTCATCATGAGTCAATAACTC	21300
Db	21241	TTTGTATCTGCTGCTATAGTACTTAAAGTCTGTGTTTCATCATGAGTCAATAACTC	21300
Qy	21301	ATAAATGCTATGATTAATACATACATCAATCAATCAATCAATCAATCAATCAATCAAT	21360
Db	21301	ATAAATGCTATGATTAATACATACATCAATCAATCAATCAATCAATCAATCAATCAAT	21360
Qy	21361	CTTTCAAAAGTTAAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	21420
Db	21361	CTTTCAAAAGTTAAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	21420
Qy	21421	GTAGAGCCAGAGTTTGAATCCAGGCTCTTTCATGCTCTTTTGTACATTTATGAGCCAGTGT	21480
Db	21421	GTAGAGCCAGAGTTTGAATCCAGGCTCTTTCATGCTCTTTTGTACATTTATGAGCCAGTGT	21480
Qy	21481	AAAGATTTGAAGGAGGTTTCAAGAGCAGCTTCCCAAGCGATGCTGAAGTCTTCCACC	21540
Db	21481	AAAGATTTGAAGGAGGTTTCAAGAGCAGCTTCCCAAGCGATGCTGAAGTCTTCCACC	21540
Qy	21541	AGAGGACCACTTGTGCTGCAAAATGACCTGCTTCTTAGGTGACCCATAGGCACTAACCT	21600
Db	21541	AGAGGACCACTTGTGCTGCAAAATGACCTGCTTCTTAGGTGACCCATAGGCACTAACCT	21600
Qy	21601	GTCAATTTTCAACAATGCTAATACACATACCAAGCAGCAGCTGTGTATCCTCATC	21660
Db	21601	GTCAATTTTCAACAATGCTAATACACATACCAAGCAGCAGCTGTGTATCCTCATC	21660
Qy	21661	CACCTATTGCTGCTGCTAATTAACAGCAGGCTATTCAGAGTCTACTTTTGTCTTGG	21720
Db	21661	CACCTATTGCTGCTGCTAATTAACAGCAGGCTATTCAGAGTCTACTTTTGTCTTGG	21720
Qy	21721	TATTGTGATAAAACATTTGCTCTTTTATCTGAACCGAGTGGACTTTGGCCAAATGACAC	21780
Db	21721	TATTGTGATAAAACATTTGCTCTTTTATCTGAACCGAGTGGACTTTGGCCAAATGACAC	21780
Qy	21781	TCTTCTCTTTTGTCTCTCAATTTTCTTGAACCCCTTTTCTTGTCTCATCTAGGAGTGAATGG	21840
Db	21781	TCTTCTCTTTTGTCTCTCAATTTTCTTGAACCCCTTTTCTTGTCTCATCTAGGAGTGAATGG	21840
Qy	21841	ATTGATAGCAATGATTTTGTCTCAGTGGGAAACAAATGCCAGGATCCTTAAAGATTTAGTT	21900
Db	21841	ATTGATAGCAATGATTTTGTCTCAGTGGGAAACAAATGCCAGGATCCTTAAAGATTTAGTT	21900
Qy	21901	TCGTGAGGACAGATAAAACCAATATATATTTTACATACATTTGGCAGCACAACATGGTG	21960
Db	21901	TCGTGAGGACAGATAAAACCAATATATATTTTACATACATTTGGCAGCACAACATGGTG	21960
Qy	21961	GTGATCAGCTTAAAGATAAAATTTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	22020
Db	21961	GTGATCAGCTTAAAGATAAAATTTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	22020
Qy	22021	TATTTATACAGTTACCTTCTGCTGGAGAGTCAAAATGTGCTTACTGGGTCAA	22080
Db	22021	TATTTATACAGTTACCTTCTGCTGGAGAGTCAAAATGTGCTTACTGGGTCAA	22080
Qy	22081	AATCAGGATATTAAGGTAAAGTCTGTTTTTGTGAATACAAAATTCATTTATGAACAAA	22140
Db	22081	AATCAGGATATTAAGGTAAAGTCTGTTTTTGTGAATACAAAATTCATTTATGAACAAA	22140

QY	22141	ATAATCTCCTCACTTTGAACATGGGAAAGCACACCTTTGTTCTCCACATGCACAAATATTTA	22200		Db	23221	AGCTACGAAGTTTCAGTAGGCTATGTGTTGAATGTGGTTTACCTAATATTTTCCA	23280	
Db	22141	ATAATCTCCTCACTTTGAACATGGGAAAGCACACCTTTGTTCTCCACATGCACAAATATTTA	22200		QY	23281	ATTACAATGTGTTTATTGGGATGTAACCCATCAAAAAGTTTAAGAGACATCCATATTCAGG	23340	
QY	22201	CTGCTTGTGTTTGGTCAACAGAGAGATGGTTTCCCTTGAGTCAGTCTCTAAACATTAAGTTA	22260		Db	23281	ATTACAATGTGTTTATTGGGATGTAACCCATCAAAAAGTTTAAGAGACATCCATATTCAGG	23340	
Db	22201	CTGCTTGTGTTTGGTCAACAGAGAGATGGTTTCCCTTGAGTCAGTCTCTAAACATTAAGTTA	22260		QY	23341	TGCTTCTCTCTTATTTGAACATAAAAAGTTGTTGGAGGTAGAGAGCTAATCATCTTTTAT	23400	
QY	22261	TCAGTTGGCTTTCACGTGCTGCCAATTCATCAATCTTTTATCTGATAGTAAACACAT	22320		Db	23341	TGCTTCTCTCTTATTTGAACATAAAAAGTTGTTGGAGGTAGAGAGCTAATCATCTTTTAT	23400	
Db	22261	TCAGTTGGCTTTCACGTGCTGCCAATTCATCAATCTTTTATCTGATAGTAAACACAT	22320		QY	23401	CCCTTCTCTCTAGTACTTTGTCCCTAATGTAAAGACCAAAATGCAGCTCAATTCAAAGCTCA	23460	
QY	22321	GCTTTTCTCTTGATCATCCACAGACTGTCAGAGAAATCCAATTAACATGCTGCATGTCC	22380		Db	23401	CCCTTCTCTCTAGTACTTTGTCCCTAATGTAAAGACCAAAATGCAGCTCAATTCAAAGCTCA	23460	
Db	22321	GCTTTTCTCTTGATCATCCACAGACTGTCAGAGAAATCCAATTAACATGCTGCATGTCC	22380		QY	23461	CTTCTAAAACCAATTTGACTTCAACGATTAGGAGCAAGGTGCTGCTGAAGGAAGCAACA	23520	
QY	22381	TTGAAGACAGTCAGTAATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	22440		Db	23461	CTTCTAAAACCAATTTGACTTCAACGATTAGGAGCAAGGTGCTGCTGAAGGAAGCAACA	23520	
Db	22381	TTGAAGACAGTCAGTAATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	22440		QY	23521	TCGCTTCTTGTGCGCAGATTTCCCTTTTCAAGAAATAGACACTCAATAATTTACTACCTGAATG	23580	
QY	22441	GCTCTGCTGCCAGGCTGGAGTGCAGTGGCATGATTTTCAGCTCACCATAACTTCCGCCCTC	22500		Db	23521	TCGCTTCTTGTGCGCAGATTTCCCTTTTCAAGAAATAGACACTCAATAATTTACTACCTGAATG	23580	
Db	22441	GCTCTGCTGCCAGGCTGGAGTGCAGTGGCATGATTTTCAGCTCACCATAACTTCCGCCCTC	22500		QY	23581	AATCAGATAAAAACCAATTTTTCAGTTTAAATTTTATCACAAAGGTGAACAATTC	23640	
QY	22501	CCAGGTTTAAAGCAATTCCTCCGCCCTCAGCCTTCTCAGTAGCTGGGACTACAGGTGTGTGC	22560		Db	23581	AATCAGATAAAAACCAATTTTTCAGTTTAAATTTTATCACAAAGGTGAACAATTC	23640	
Db	22501	CCAGGTTTAAAGCAATTCCTCCGCCCTCAGCCTTCTCAGTAGCTGGGACTACAGGTGTGTGC	22560		QY	23641	AACTATCTTTCAGGAATGCATAGAGTATTAATACTTTATATCTTGAATCTTTTGGATC	23700	
QY	22561	CACATGCCAGCTAATTTTGTATTTTTCATTAGAGATAGAGTTTCACCATGTTGGCACC	22620		Db	23641	AACTATCTTTCAGGAATGCATAGAGTATTAATACTTTATATCTTGAATCTTTTGGATC	23700	
Db	22561	CACATGCCAGCTAATTTTGTATTTTTCATTAGAGATAGAGTTTCACCATGTTGGCACC	22620		QY	23701	TTATCTCAAGACTAGTCTAGGATGTTGTCGCAAGTGTAGTGGTAAAGTTAGAAATTAAGAA	23760	
QY	22621	GTAATCATTTTATTTGTTTACAAGGCTFAGGCTTTTATAATGCTAAAGTCTCTTTATAAC	22680		Db	23701	TTATCTCAAGACTAGTCTAGGATGTTGTCGCAAGTGTAGTGGTAAAGTTAGAAATTAAGAA	23760	
Db	22621	GTAATCATTTTATTTGTTTACAAGGCTFAGGCTTTTATAATGCTAAAGTCTCTTTATAAC	22680		QY	23761	ACTAGGATTTAGAACCATCTCTGCCAAGATGAACCAAGATGCATGAGTACTGGCACC	23820	
QY	22681	TCTTAGCAGGCATGAGCAGCAGCCTACATACCTAGTGCATATTTACCACATGGTGTATGC	22740		Db	23761	ACTAGGATTTAGAACCATCTCTGCCAAGATGAACCAAGATGCATGAGTACTGGCACC	23820	
Db	22681	TCTTAGCAGGCATGAGCAGCAGCCTACATACCTAGTGCATATTTACCACATGGTGTATGC	22740		QY	23821	AAGATCTCTGAAATATAGGAGTGGCAGACATGGTGAAGACATGCTTGTGAGAGACGTGGTT	23880	
QY	22741	ATGTGGAGATGAGCAGCTCAAAAGTAGGGCCATGATGTTTTTGAACACCATGCTTGTGTC	22800		Db	23821	AAGATCTCTGAAATATAGGAGTGGCAGACATGGTGAAGACATGCTTGTGAGAGACGTGGTT	23880	
Db	22741	ATGTGGAGATGAGCAGCTCAAAAGTAGGGCCATGATGTTTTTGAACACCATGCTTGTGTC	22800		QY	23881	CTCAGATCAAAACATCAAGGTGCTAAGGAACATTCCTCTTGTCAAAATGGGAGACAGTGCC	23940	
QY	22801	TTCTGTTTGTCTTCTGGCATCTCAGCTTGCATATATATTTTAACTCTCTAGAGCTCA	22860		Db	23881	CTCAGATCAAAACATCAAGGTGCTAAGGAACATTCCTCTTGTCAAAATGGGAGACAGTGCC	23940	
Db	22801	TTCTGTTTGTCTTCTGGCATCTCAGCTTGCATATATATTTTAACTCTCTAGAGCTCA	22860		QY	23941	ATAATCTGTTATGAAAAAGTGCCTAAACATTTCCCTTTAATGTTGCAGCACCAGGTTTATGA	24000	
QY	22861	AGTCAAAAGGCATATTCACCTACATCTCCTATGACTCCCTCTATGCTATGCTACACACAC	22920		Db	23941	ATAATCTGTTATGAAAAAGTGCCTAAACATTTCCCTTTAATGTTGCAGCACCAGGTTTATGA	24000	
Db	22861	AGTCAAAAGGCATATTCACCTACATCTCCTATGACTCCCTCTATGCTATGCTACACACAC	22920		QY	24001	TGCTTTGGGGTGGGTGGGAGTGAAGGAGCTATAGGAAATAAATCTATTTTGTGTTAA	24060	
QY	22921	TTTTCTGCCCCTTATATAGCATTTACTTTCAATAGACCTTTGTTGTTTCTTCTTCAGAT	22980		Db	24001	TGCTTTGGGGTGGGTGGGAGTGAAGGAGCTATAGGAAATAAATCTATTTTGTGTTAA	24060	
Db	22921	TTTTCTGCCCCTTATATAGCATTTACTTTCAATAGACCTTTGTTGTTTCTTCTTCAGAT	22980		QY	24061	ACAACAGGGGCTCTCAGCCCTTCTCAAGGTTCTAAGTTCACAGGAGTCTTCATCCCT	24120	
QY	22981	AGTCCAACCTACAATGGTTCAACATGAGTTTTTTTTTTTTTACTTTTTTGTATGGTCTTTC	23040		Db	24061	ACAACAGGGGCTCTCAGCCCTTCTCAAGGTTCTAAGTTCACAGGAGTCTTCATCCCT	24120	
Db	22981	AGTCCAACCTACAATGGTTCAACATGAGTTTTTTTTTTTTTACTTTTTTGTATGGTCTTTC	23040		QY	24121	ATGAATATACAACTCTCACTGTGATTTTTCAGAAATCCCTCTCTCTATATAATCAGCACAAT	24180	
QY	23041	AGCTGTGATGTTAATGGTGAGCACCACCAATAAACCATTCCTGTTTTTCTCTTTCAGTAAG	23100		Db	24121	ATGAATATACAACTCTCACTGTGATTTTTCAGAAATCCCTCTCTCTATATAATCAGCACAAT	24180	
Db	23041	AGCTGTGATGTTAATGGTGAGCACCACCAATAAACCATTCCTGTTTTTCTCTTTCAGTAAG	23100		QY	24181	TATGAAAACTGTTTTTACATTTTCAATCCCAATGCAAGAGTGCATAATCTGGAAGGA	24240	
QY	23101	TATTCATAAATATATAGCTATTAAACCTCTATTATAAATAAGGCTTTGTTGGTAGATA	23160		Db	24181	TATGAAAACTGTTTTTACATTTTCAATCCCAATGCAAGAGTGCATAATCTGGAAGGA	24240	
Db	23101	TATTCATAAATATATAGCTATTAAACCTCTATTATAAATAAGGCTTTGTTGGTAGATA	23160		QY	24241	CAATTTATTTTAAAGTTTAAATAGGGAGTATCAGGATACTTTAACTTTAAATATGAAA	24300	
QY	23161	ATACCTGACCAACTATAGGCTGATATATGCGTTTCTGAACATGTTTAAAGTAGGCTAGGCTT	23220		Db	24241	CAATTTATTTTAAAGTTTAAATAGGGAGTATCAGGATACTTTAACTTTAAATATGAAA	24300	
Db	23161	ATACCTGACCAACTATAGGCTGATATATGCGTTTCTGAACATGTTTAAAGTAGGCTAGGCTT	23220		QY	24301	GACACTGAATTTTGTGACTCCACATGTCGGTTTAACTCTTAAAGATAAAAAACATTTTACC	24360	
QY	23221	AGCTACGAAGTTTCAGTAGGCTATGTGTTGAATGTGGTTTACCTAATATTTTCCA	23280						

Db	24301	GACACTGAAATTTTGTGACTCCACATGTGGGTTTAAACATCTAAAGAATAAAAAAATTTACC	24360
QY	24361	ACTTGTGTTTTACACAAATTAACCTAAATCACAGCAAAAGATTCTTAATCAGACAATTTCT	24420
Db	24361	ACTTGTGTTTTACACAAATTAACCTAAATCACAGCAAAAGATTCTTAATCAGACAATTTCT	24420
QY	24421	GATTTTCAGGTTTAGAAGCATTTGTAAGCAAGGAGTGAATGCAAACTTTACTGAGCAACT	24480
Db	24421	GATTTTCAGGTTTAGAAGCATTTGTAAGCAAGGAGTGAATGCAAACTTTACTGAGCAACT	24480
QY	24481	ACTATCTATCCAGCACTTTGTGAGATGCTTTCACAAAAATCAAAATTTCAATTTCTCAC	24540
Db	24481	ACTATCTATCCAGCACTTTGTGAGATGCTTTCACAAAAATCAAAATTTCAATTTCTCAC	24540
QY	24541	AGCAAAACCTCATCTTTAGATATTACAAATTCCTCCATTCGATGGATGATAGAACTGAGTTGCA	24600
Db	24541	AGCAAAACCTCATCTTTAGATATTACAAATTCCTCCATTCGATGGATGATAGAACTGAGTTGCA	24600
QY	24601	GAGGACTTAAGTGACTTTGGCTTAAGCCACTGGACGTAAGTAGATATTCAGCACATATGTA	24660
Db	24601	GAGGACTTAAGTGACTTTGGCTTAAGCCACTGGACGTAAGTAGATATTCAGCACATATGTA	24660
QY	24661	CTGGAAAAATCAATGGATGACTGAATGAATATCTGGAAGGCACCTGAATTAGCCATGAAGC	24720
Db	24661	CTGGAAAAATCAATGGATGACTGAATGAATATCTGGAAGGCACCTGAATTAGCCATGAAGC	24720
QY	24721	AGTAACACCATCATAAAGCCATTCTCTGAACCTCGGAATTCATGACCTGGGGTGATGTA	24780
Db	24721	AGTAACACCATCATAAAGCCATTCTCTGAACCTCGGAATTCATGACCTGGGGTGATGTA	24780
QY	24781	TAAAGCATATCTATGAANAATGAAAAATTTTTTAAAAAACAAGTTAGGAGATGAAGGTCCTTA	24840
Db	24781	TAAAGCATATCTATGAANAATGAAAAATTTTTTAAAAAACAAGTTAGGAGATGAAGGTCCTTA	24840
QY	24841	AAATTTCTTGTTCTCATTTTACTAGACTATGAATGAATCCCTGAGCTTTAAACACCATTTGATTTG	24900
Db	24841	AAATTTCTTGTTCTCATTTTACTAGACTATGAATGAATCCCTGAGCTTTAAACACCATTTGATTTG	24900
QY	24901	CTCACAGCATGAGCTTTGCGAGCAACAAGCCCAAGTTTCATGTCATGATTTCTTATTTTCT	24960
Db	24901	CTCACAGCATGAGCTTTGCGAGCAACAAGCCCAAGTTTCATGTCATGATTTCTTATTTTCT	24960
QY	24961	AGCTCTCAGAAACCTTCTGAATTTTTTCTTTTACTATGCAAAAATGGGAATCACAGTA	25020
Db	24961	AGCTCTCAGAAACCTTCTGAATTTTTTCTTTTACTATGCAAAAATGGGAATCACAGTA	25020
QY	25021	GCCTCTGCCAAGGAACCTGTTAAGATTAAATGAGTTTTCAGTGTGTTTGAAGCACAGTCTTA	25080
Db	25021	GCCTCTGCCAAGGAACCTGTTAAGATTAAATGAGTTTTCAGTGTGTTTGAAGCACAGTCTTA	25080
QY	25081	AATCTTACCTCTCAGTAGGTATGCCACATTTATTTACTGAAGTGAGTAAACAAAAAGCCATGATCAGG	25140
Db	25081	AATCTTACCTCTCAGTAGGTATGCCACATTTATTTACTGAAGTGAGTAAACAAAAAGCCATGATCAGG	25140
QY	25141	AAGGAAGTTTAAATCAGAGCACCTTAAACTAGAGGAGCTGAGATTCGTAAATGGTGA	25200
Db	25141	AAGGAAGTTTAAATCAGAGCACCTTAAACTAGAGGAGCTGAGATTCGTAAATGGTGA	25200
QY	25201	TTACTAAGGAATAGAGGCCATGCCACCTTGAACTTAATACAAAAAGCCATGATCAGG	25260
Db	25201	TTACTAAGGAATAGAGGCCATGCCACCTTGAACTTAATACAAAAAGCCATGATCAGG	25260
QY	25261	TGCTTTTCAGTTTATACATCAGACGTAACACTATCTTTGCAAGTGATTTAGTCCATTC	25320
Db	25261	TGCTTTTCAGTTTATACATCAGACGTAACACTATCTTTGCAAGTGATTTAGTCCATTC	25320
QY	25321	TCATCTGAGATAAAGAACCCCAAGACTGGGTAGTTTATAAAGAAAAAGAGGTTTAAATG	25380
Db	25321	TCATCTGAGATAAAGAACCCCAAGACTGGGTAGTTTATAAAGAAAAAGAGGTTTAAATG	25380
QY	25381	GCCTCACAGTTATGCAATTCCTGGGAGGCCCTAAGGAACTTACATCATCTGGCAGAGCGG	25440
Db	25381	GCCTCACAGTTATGCAATTCCTGGGAGGCCCTAAGGAACTTACATCATCTGGCAGAGCGG	25440
QY	25441	AAGGAGAACAAAGGCACCTCTTACATGCTGGCAGGAGGAGCATCTGTGCAAGTGTA	25500
Db	25441	AAGGAGAACAAAGGCACCTCTTACATGCTGGCAGGAGGAGCATCTGTGCAAGTGTA	25500
QY	25501	GGGGAACCTCCCTTTATAAATCATCAGATCTTGTGCCACTCCTCCTCATCATCACAAGAT	25560
Db	25501	GGGGAACCTCCCTTTATAAATCATCAGATCTTGTGCCACTCCTCCTCATCATCACAAGAT	25560
QY	25561	AGCATGGGGAACCACTCCCATGATTCAATATCTCCATCTTGTTCCTCCTTGACATG	25620
Db	25561	AGCATGGGGAACCACTCCCATGATTCAATATCTCCATCTTGTTCCTCCTTGACATG	25620
QY	25621	TGGGGAATTATGGGATTATGGGATTGCAATTCAGATGAGATTTGGGTGGGAGACAAAT	25680
Db	25621	TGGGGAATTATGGGATTATGGGATTGCAATTCAGATGAGATTTGGGTGGGAGACAAAT	25680
QY	25681	GCATACTATATAGCAAGTAAAGACACTCAGTGAGTTGGATCTCTCAGCACACGAGG	25740
Db	25681	GCATACTATATAGCAAGTAAAGACACTCAGTGAGTTGGATCTCTCAGCACACGAGG	25740
QY	25741	CCTACAAGCATATATCTCTAGGAGCAGTGTAGTGTCTCCTTAAAGTCTAGTGGGCATAA	25800
Db	25741	CCTACAAGCATATATCTCTAGGAGCAGTGTAGTGTCTCCTTAAAGTCTAGTGGGCATAA	25800
QY	25801	AGGAAACCAATCCCATTAATTTTCCAATGCTTCCAGAAAAAATTTAGCACAGCAAAAC	25860
Db	25801	AGGAAACCAATCCCATTAATTTTCCAATGCTTCCAGAAAAAATTTAGCACAGCAAAAC	25860
QY	25861	ACAAGAACACACATTTCTCTTTAAACAAGTAATTTGCAAGTGAATAATGCACATTTGTTC	25920
Db	25861	ACAAGAACACACATTTCTCTTTAAACAAGTAATTTGCAAGTGAATAATGCACATTTGTTC	25920
QY	25921	ATCCGAGCGTAAAAGTTTACCTATGGCTTCCACTGTCAACTGGATTTTCCCTATTGATTT	25980
Db	25921	ATCCGAGCGTAAAAGTTTACCTATGGCTTCCACTGTCAACTGGATTTTCCCTATTGATTT	25980
QY	25981	GCATTTGAATGACATCCCTAGATGAGGGAATAACTTTGATATAGGGTGGGGTTAGGA	26040
Db	25981	GCATTTGAATGACATCCCTAGATGAGGGAATAACTTTGATATAGGGTGGGGTTAGGA	26040
QY	26041	TATCCACAAAGAGCGCAACTGGCTAGATGAAAGAGAGAGTGCCACAGGACACAGGA	26100
Db	26041	TATCCACAAAGAGCGCAACTGGCTAGATGAAAGAGAGAGTGCCACAGGACACAGGA	26100
QY	26101	GGAAAAACAACCTGAAAGTTGTCCACTGCTGAGATTTCTTAAATATTTTCATGCTGTG	26160
Db	26101	GGAAAAACAACCTGAAAGTTGTCCACTGCTGAGATTTCTTAAATATTTTCATGCTGTG	26160
QY	26161	CCCTCATAGACACACAAATATGATAAACAACAATATGTTTATGAATGCTTGTGTC	26220
Db	26161	CCCTCATAGACACACAAATATGATAAACAACAATATGTTTATGAATGCTTGTGTC	26220
QY	26221	AAACAGAGTAAGTGAGGAGCTAGATACCTTACAATCATATGAGTCAATACAGTGGCAA	26280
Db	26221	AAACAGAGTAAGTGAGGAGCTAGATACCTTACAATCATATGAGTCAATACAGTGGCAA	26280
QY	26281	AGTCTCTAAAAGAAAAGCTTAGCAGAAAAACCATCAATAGCAAAATAGTGTGAGAA	26340
Db	26281	AGTCTCTAAAAGAAAAGCTTAGCAGAAAAACCATCAATAGCAAAATAGTGTGAGAA	26340
QY	26341	ATTCTCGGATAAATAGTATCAGAAAAAGTTTAGTACTTGGAGATAATTTTGAACCTTTTA	26400
Db	26341	ATTCTCGGATAAATAGTATCAGAAAAAGTTTAGTACTTGGAGATAATTTTGAACCTTTTA	26400
QY	26401	ATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTGGCAAAATCTATCTGTG	26460
Db	26401	ATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTGGCAAAATCTATCTGTG	26460
QY	26461	AGGCTCTCCAGATTACTGATGGTTATCTTTAGAGCCCTTATAGGGAAGACAGACAGCAAT	26520
Db	26461	AGGCTCTCCAGATTACTGATGGTTATCTTTAGAGCCCTTATAGGGAAGACAGACAGCAAT	26520

QY	26521	AATAGAAATATCTTGGTCTCTGTCAGAGTTTTGCAAGCAATTCAAATAATAACAGTAGCT	26580		Db	27601	ATGTTTACTGCACTCAATATTAAATACTGTTTTTTTCTGTTGTTTTTTT	27660
Db	26521	AATAGAAATATCTTGGTCTCTGTCAGAGTTTTGCAAGCAATTCAAATAATAACAGTAGCT	26580		QY	27661	TTTTTAAAGCAGGGTCTTCACTCTGTTGACAGAGCTGAGTCCAGTGGTGCAGTCCACAGC	27720
QY	26581	ATCATTTATTGAGGGTGTAGATACCTTTTCATTACCTTAACACAAATTTGCAAA	26640		Db	27661	TTTTTAAAGCAGGGTCTTCACTCTGTTGACAGAGCTGAGTGGTGCAGTCCACAGC	27720
Db	26581	ATCATTTATTGAGGGTGTAGATACCTTTTCATTACCTTAACACAAATTTGCAAA	26640		QY	27721	CCATGGTAGCCTTGAACCTACCGGGCTCAAGTGAFTCCACCCTCCAGCCTCCTCAGTAG	27780
QY	26641	GTGCTTTATAATTAGAGCCATTTTACAAAGAGAGAAATFAGAGATCAGGGGTCTGTAAG	26700		Db	27721	CCATGGTAGCCTTGAACCTACCGGGCTCAAGTGAFTCCACCCTCCTCAGTAG	27780
Db	26641	GTGCTTTATAATTAGAGCCATTTTACAAAGAGAGAAATFAGAGATCAGGGGTCTGTAAG	26700		QY	27781	CTGGAACCTACAGGTATATGCTTCACGCTGGCTAACTTTTGTATTTTGTAGACAGAGG	27840
QY	26701	TGACTTCTCCAAAGGCCACTGCTACTGATTTTAGGATTTGAGTGTAGAAATTTTATACAAGT	26760		Db	27781	CTGGAACCTACAGGTATATGCTTCACGCTGGCTAACTTTTGTATTTTGTAGACAGAGG	27840
Db	26701	TGACTTCTCCAAAGGCCACTGCTACTGATTTTAGGATTTGAGTGTAGAAATTTTATACAAGT	26760		QY	27841	TTCCTCACCATTGTCGCCAGGCTGGTCTCTCACTCCCTGGGCTCAAGGATCTGCCCTACCTC	27900
QY	26761	TAGTTTGACTCTCAAGTCCATGCTCTTTCCATTGCAAGCTGCTCTTCTTTTGTCTCTAT	26820		Db	27841	TTCCTCACCATTGTCGCCAGGCTGGTCTCTCACTCCCTGGGCTCAAGGATCTGCCCTACCTC	27900
Db	26761	TAGTTTGACTCTCAAGTCCATGCTCTTTCCATTGCAAGCTGCTCTTCTTTTGTCTCTAT	26820		QY	27901	GGCCTCCCAAAAGTGTGGGATCAGAGCAGTGAAGCAGCTGTGTCGAGTCTAAACACTTTT	27960
QY	26821	TTCTATTAAATTTATGCCAAACAATTTTAAATATTCATAAATAAAACTTTCACTTGGTAAA	26880		Db	27901	GGCCTCCCAAAAGTGTGGATCAGAGCAGTGAAGCAGCTGTGTCGAGTCTAAACACTTTT	27960
Db	26821	TTCTATTAAATTTATGCCAAACAATTTTAAATATTCATAAATAAAACTTTCACTTGGTAAA	26880		QY	27961	TAAAGAGAGGTGGATTTGAATTTTAGCATGTGTATCTAAATAATGATTTTCTGGAGA	28020
QY	26881	GGTACCAATATPACACATGTTTCAGGAAACTCAATGAAGCTAACCATCTTTTCAATAATA	26940		Db	27961	TAAAGAGAGGTGGATTTGAATTTTAGCATGTGTATCTAAATAATGATTTTCTGGAGA	28020
Db	26881	GGTACCAATATPACACATGTTTCAGGAAACTCAATGAAGCTAACCATCTTTTCAATAATA	26940		QY	28021	ACAATATATTTTAAATTTTAAACTATTAATTTTGGAACTACCCCAATAATTTCTGT	28080
QY	26941	GAACTATTTTAAACAATATGTAATATTAATGAACACACAGTTTATTAATGTCCTA	27000		Db	28021	ACAATATATTTTAAATTTTAAACTATTAATTTTGGAACTACCCCAATAATTTCTGT	28080
Db	26941	GAACTATTTTAAACAATATGTAATATTAATGAACACACAGTTTATTAATGTCCTA	27000		QY	28081	CATATTTTAAATCAAAACACAGCTTTGAAAACAGGTTTCCCTCTTGCCTATATGTCCTG	28140
QY	27001	TTATCTACTGATGTCCACAGTACCCTTAAATTTACAGAGATGTAGTTACAGATATCTGA	27060		Db	28081	CATATTTTAAATCAAAACACAGCTTTGAAAACAGGTTTCCCTCTTGCCTATATGTCCTG	28140
Db	27001	TTATCTACTGATGTCCACAGTACCCTTAAATTTACAGAGATGTAGTTACAGATATCTGA	27060		QY	28141	GATTTTCTCTTGGTGAACACACTATCATCTTAGAAGTCAAGTCTCTCGAATAAGAAA	28200
QY	27061	AGACTGACTGATCTGACTCATCATCTGCTGGCCCAACAGCTTTTGGCAAAATCTTAACC	27120		Db	28141	GATTTTCTCTTGGTGAACACACTATCATCTTAGAAGTCAAGTCTCTCGAATAAGAAA	28200
Db	27061	AGACTGACTGATCTGACTCATCATCTGCTGGCCCAACAGCTTTTGGCAAAATCTTAACC	27120		QY	28201	AAGAACAGATCTTACTTATATTTATCTCCATAAATCAGCTCTCCGTTAATGCCAGT	28260
QY	27121	CAAGTATCAAAATAGCAGACAGAGAAATTCGAACACTCAGTTTCTAAATATGTTCTAT	27180		Db	28201	AAGAACAGATCTTACTTATATTTATCTCCATAAATCAGCTCTCCGTTAATGCCAGT	28260
Db	27121	CAAGTATCAAAATAGCAGACAGAGAAATTCGAACACTCAGTTTCTAAATATGTTCTAT	27180		QY	28261	CAGGCTGATCATTTCTTAAATTTAGAAATGTGAAATTTATGCTATGAATTTGAATAAT	28320
QY	27181	ATGTTAATGCTCTCTGAATAATTTCTTACATTTGAAATCAITTTTGAATAATTTT	27240		Db	28261	CAGGCTGATCATTTCTTAAATTTAGAAATGTGAAATTTATGCTATGAATTTGAATAAT	28320
Db	27181	ATGTTAATGCTCTCTGAATAATTTCTTACATTTGAAATCAITTTTGAATAATTTT	27240		QY	28321	ATACATGTCCTTAAATTCATAGGTATATGTTTTTCTGTTTTGTTTTTTTTTAAT	28380
QY	27241	GTGTCCTCTGTTTAGCATGCAATGAGTGAACAGCAATGAATAAATTT	27300		Db	28321	ATACATGTCCTTAAATTCATAGGTATATGTTTTTCTGTTTTGTTTTTTTTTAAT	28380
Db	27241	GTGTCCTCTGTTTAGCATGCAATGAGTGAACAGCAATGAATAAATTT	27300		QY	28381	TTATGATTATTTACTTTAAGTTTTAGAGTACATATGCACAAATGTCAGAGTTTGTACAT	28440
QY	27301	TTTTAAAGAACCTATCTGACTTTAGAGAACTCAGAACGAATGAATAATCTGATATAA	27360		Db	28381	TTATGATTATTTACTTTAAGTTTTAGAGTACATATGCACAAATGTCAGAGTTTGTACAT	28440
Db	27301	TTTTAAAGAACCTATCTGACTTTAGAGAACTCAGAACGAATGAATAATCTGATATAA	27360		QY	28441	ATGATACATGTGCCATGTTGGTGTGCCACCATTAACCTGCTCATTTAAACATTTAGTA	28500
QY	27361	AACATTTATTTTCTTCTCAGTTTCTTATGCTAGTATTTTACCTGTAATAATTTG	27420		Db	28441	ATGATACATGTGCCATGTTGGTGTGCCACCATTAACCTGCTCATTTAAACATTTAGTA	28500
Db	27361	AACATTTATTTTCTTCTCAGTTTCTTATGCTAGTATTTTACCTGTAATAATTTG	27420		QY	28501	TATCTCTTAATGCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	28560
QY	27421	CAAAATAGAGTCAAAATGTTTAGATTTTAGAGGAAATGTCATGGAGAAATAATAGAAAT	27480		Db	28501	TATCTCTTAATGCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	28560
Db	27421	CAAAATAGAGTCAAAATGTTTAGATTTTAGAGGAAATGTCATGGAGAAATAATAGAAAT	27480		QY	28561	GTTCCCTCTCTGTGTCCTCATGTTCTCATTTGTTCAATTCACCACTATGAGTGAAGAACAT	28620
QY	27481	TGGTATTAGCTTCCCTGGAAATGGTGGTGAAGTTCACAGTGTCTAACATCTAACCAT	27540		Db	28561	GTTCCCTCTCTGTGTCCTCATGTTCTCATTTGTTCAATTCACCACTATGAGTGAAGAACAT	28620
Db	27481	TGGTATTAGCTTCCCTGGAAATGGTGGTGAAGTTCACAGTGTCTAACATCTAACCAT	27540		QY	28621	CGGCTGTTGTTTTTGTCTCTGTGATGTTGCTGAGAAATGATGTTTCCAGCTTCAT	28680
QY	27541	TAGAGTCTGTAATAATCACATATTTCAACAGCTCATCTTTGGAACATAATTTAGTATCAAG	27600		Db	28621	CGGCTGTTGTTTTTGTCTCTGTGATGTTGCTGAGAAATGATGTTTCCAGCTTCAT	28680
Db	27541	TAGAGTCTGTAATAATCACATATTTCAACAGCTCATCTTTGGAACATAATTTAGTATCAAG	27600		QY	28681	CCATGTCCTCAAAAGGACGAACTCATCTTTTATGCTGCTCATGATTTCCATGCT	28740
QY	27601	ATGTTTACTGCACTCAATATTAAATACTGTTTTTTGTTGTTTTTTTTT	27660					

Db 1312 CAGGCTAGTAGTAAGTTGGTGGTAGGAAAGGGTCTTATCTCACCCCTCTTAA 1253
QY 481 ACTAAAGGTCTTTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGGTCTT 540
Db 1252 ACTAAAGGTCTTTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGGTCTT 1193
QY 541 GAGCTGCAGATACAATACATCGTTTCATGTTGATCCAACTGGATGTCAACTAGAGCCATG 600
Db 1192 GAGCTGCAGATACAATACATCGTTTCATGTTGATCCAACTGGATGTCAACTAGAGCCATG 1133
QY 601 GTCTTAGCTCTACCCCTCTCTGTATGTGGCCAGGCTCAAACTGTAATACCT 652
Db 1132 GTCTTAGCTCTACCCCTCTCTGTATGTGGCCAGGCTCAAACTGTAATACCT 1081

RESULT 3

US-10-258-557-1/c

Sequence: US258557
Publication No. US20030100502AT
GENERAL INFORMATION:

APPLICANT: Beals, John
APPLICANT: Gonzalez-DeWhitt, Patricia
APPLICANT: Hammond, Lisa
APPLICANT: Lu, Jirong
APPLICANT: Na, Songqing
APPLICANT: Su, Eric
APPLICANT: Witcher, Derrick
TITLE OF INVENTION: TREATING MUSCULOSKELETAL DISORDERS USING LP85 AND ANALOGS THEREOF
FILE REFERENCE: X-14392M
CURRENT APPLICATION NUMBER: US/10/258,557
CURRENT FILING DATE: 2002-10-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3736
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (114)..(1223)
FEATURE: sig_peptide
NAME/KEY: (114)..(149)
LOCATION: (114)..(149)
US-10-258-557-1

Query Match 2.2%; Score 652; DB 9; Length 3736;

Best Local Similarity 100.0%; Pred. No. 1.3e-285; Mismatches 0; Indels 0; Gaps 0;

Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 60
Db 1750 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 1691
QY 61 GCAAGATTCAAAATTTGTTTGTTCAAAATTTTAAATATATATCTCTCTAAATTTT 120
Db 1690 GCAAGATTCAAAATTTGTTTGTTCAAAATTTTAAATATATATCTCTCTAAATTTT 1631
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGCAAGGATTTTAAGAGTCT 180
Db 1630 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGCAAGGATTTTAAGAGTCT 1571
QY 181 AACTCAACATATGTAAGCTCTGTTGTTACCTGTTATATACCAAAAAACATTTGAT 240
Db 1570 AACTCAACATATGTAAGCTCTGTTGTTACCTGTTATATACCAAAAAACATTTGAT 1511
QY 241 CTAATACACATAGACATGAATATATTTCTGTGTGTTTGTGTCATATATACCTCAAC 300
Db 1510 CTAATACACATAGACATGAATATATTTCTGTGTGTTTGTGTCATATATACCTCAAC 1451
QY 301 ACTATATTAATGCAATCCCTATATCTTAGGTATAGAGTTGATGATATACCTTCTAC 360
Db 1450 ACTATATTAATGCAATCCCTATATCTTAGGTATAGAGTTGATGATATACCTTCTAC 1391

RESULT 4

US-10-086-623-5/c

Sequence: US Application US/10086623
Publication No. US2002016740A1
GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LI, Xuri
APPLICANT: PONTE, Annica
APPLICANT: UTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES
FILE REFERENCE: 1064/44833C2
CURRENT APPLICATION NUMBER: US/10/086,623
CURRENT FILING DATE: 2000-03-04
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 09/691,200
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 1934
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(966)
OTHER INFORMATION:
US-10-086-623-5

Query Match

2.0%; Score 601; DB 9; Length 1934;

Best Local Similarity 99.8%; Pred. No. 2e-262;
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 60
Db 1493 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 1434

QY 61 GCAAGATCAAAATGTTTGGTTCCTTCAAAATTTAAATTTATCTCTCTAAATTTT 120
Db 1433 GCAAGATCAAAATGTTTGGTTCCTTCAAAATTTAAATTTATCTCTCTAAATTTT 1374
QY 121 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGGATTTTAAAGAGTCT 180
Db 1373 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGGATTTTAAAGAGTCT 1314
QY 181 AACTCAACATATGTAAGCTCTGGTACCTGTTATATATACCAAAAAACATTTGAT 240
Db 1313 AACTCAACATATGTAAGCTCTGGTACCTGTTATATATACCAAAAAACATTTGAT 1254
QY 241 CTATATACATAGACATGAATATATTTCTGTGTGTTTGGCATATATAACCTCAAC 300
Db 1253 CTATATACATAGACATGAATATATTTCTGTGTGTTTGGCATATATAACCTCAAC 1194
QY 301 ACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGATACCTTTCTAC 360
Db 1193 ACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGATACCTTTCTAC 1134
QY 361 TTGCCATGCAATTAACAAAGCAAGGCTGAGACTCAGCAACCACTTTGTTGATGCTTG 420
Db 1133 TTGCCATGCAATTAACAAAGCAAGGCTGAGACTCAGCAACCACTTTGTTGATGCTTG 1074
QY 421 CAGGCTAGTAGTAAGTTTGGTGTGCTAGGAAAGGGTCTCTTATCTCACCTCTCTAA 480
Db 1073 CAGGCTAGTAGTAAGTTTGGTGTGCTAGGAAAGGGTCTCTTATCTCACCTCTCTAA 1014
QY 481 ACTAAGGTTCTTTTCAGGCTTAATGTAAGGATGTCACATTTCTTATCGAGTGTCTTT 540
Db 1013 ACTAAGGTTCTTTTCAGGCTTAATGTAAGGATGTCACATTTCTTATCGAGTGTCTTT 954
QY 541 GAGCTGCAGATACATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 953 GAGCTGCAGATACATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 894
QY 601 GTCTTAGCTCTACCCCTCTCTGTGATGTCGCCAGGCTCAAACTGTAATACCT 652
Db 893 GTCTTAGCTCTACCCCTCTCTGTGATGTCGCCAGGCTCAAACTGTAATACCT 842

RESULT 5

US-10-260-539-5/c
; Sequence 5, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/260,539
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200

; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(966)
; OTHER INFORMATION:
US-10-260-539-5

Query Match 2.0%; Score 601; DB 9; Length 1934;
Best Local Similarity 99.8%; Pred. No. 2e-262; 1; Indels 0; Gaps 0;
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCTCATCTTTGATTTTAAATATATACAGATGCTTTCTTTAAAGAGA 60
Db 1493 GTATATGTAAGAAAGCCTCATCTTTGATTTTAAATATATACAGATGCTTTCTTTAAAGAGA 1434
QY 61 GCAAGATTCACAAATGTTTGTGTTTCAAAATTTAAATTTATCTCTCTAAATTTT 120
Db 1433 GCAAGATTCACAAATGTTTGTGTTTCAAAATTTAAATTTATCTCTCTAAATTTT 1374
QY 121 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGGATTTTAAAGAGTCT 180
Db 1373 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGGATTTTAAAGAGTCT 1314
QY 181 AACTCAACATATGTAAGCTCTGGTGTGCTGATATATATACCAAAAAACATTTGAT 240
Db 1313 AACTCAACATATGTAAGCTCTGGTGTGCTGATATATATACCAAAAAACATTTGAT 1254
QY 241 CTATATACATAGACATGAATATATTTCTGTGTGTTTGGCATATATAACCTCAAC 300
Db 1253 CTATATACATAGACATGAATATATTTCTGTGTGTTTGGCATATATAACCTCAAC 1194
QY 301 ACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGATACCTTTCTAC 360
Db 1193 ACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGATACCTTTCTAC 1134
QY 361 TTGCCATGCAATTAACAAAGCAAGGCTGAGACTCAGCAACCACTTTGTTGATGCTTG 420
Db 1133 TTGCCATGCAATTAACAAAGCAAGGCTGAGACTCAGCAACCACTTTGTTGATGCTTG 1074
QY 421 CAGGCTAGTAGTAAGTTTGGTGTGCTAGGAAAGGGTCTCTTATCTCACCTCTCTAA 480
Db 1073 CAGGCTAGTAGTAAGTTTGGTGTGCTAGGAAAGGGTCTCTTATCTCACCTCTCTAA 1014
QY 481 ACTAAGGTTCTTTTCAGGCTTAATGTAAGGATGTCACATTTCTTATCGAGTGTCTTT 540
Db 1013 ACTAAGGTTCTTTTCAGGCTTAATGTAAGGATGTCACATTTCTTATCGAGTGTCTTT 954
QY 541 GAGCTGCAGATACATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 953 GAGCTGCAGATACATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 894
QY 601 GTCTTAGCTCTACCCCTCTCTGTGATGTCGCCAGGCTCAAACTGTAATACCT 652
Db 893 GTCTTAGCTCTACCCCTCTCTGTGATGTCGCCAGGCTCAAACTGTAATACCT 842

RESULT 6

US-10-086-623-7/c
; Sequence 7, Application US/10086623
; Patent No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari

```

; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086.623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)..(1288)
; OTHER INFORMATION:
; US-10-086-623-7

```

Query Match	2.08;	Score 601;	DB 9;	Length 2253;
Best Local Similarity	99.98;	Pred. No. 2e-262;		
Matches 651;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	GTATATGTAAGAAGCCTCATCTTTTGATTTTTAAATACAAGATGCTTTCTTTAAAGAGA	60	
DB	1812	GTATATGTAAGAAGCCTCATCTTTTGATTTTTAAATACAAGATGCTTTCTTTAAAGAGA	1753	
QY	61	GCAAGATTCAAAATGTTTTGCTTCAAAATTTAAAAATAAATTTATCTCCTAAATTTT	120	
DB	1752	GCAAGATTCAAAATGTTTTGCTTCAAAATTTAAAAATAAATTTATCTCCTAAATTTT	1693	
QY	121	CTAAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT	180	
DB	1692	CTAAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT	1633	
QY	181	AACTCAAAACATATGTAAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACAATTTGAT	240	
DB	1632	AACTCAAAACATATGTAAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACAATTTGAT	1573	
QY	241	CTATATACATATAGACATGAATATATTTCTGTGTGTGTGTGCATATATAAAGCTCAAAAC	300	
DB	1572	CTATATACATATAGACATGAATATATTTCTGTGTGTGTGTGCATATATAAAGCTCAAAAC	1513	
QY	301	ACTATTTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC	360	
DB	1512	ACTATTTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC	1453	
QY	361	TTGCCATGGCATTTAAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTTGTTCAATTCGATTG	420	
DB	1452	TTGCCATGGCATTTAAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTTGTTCAATTCGATTG	1393	
QY	421	CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGTCCTTATCTCACCTTCCTTAA	480	
DB	1392	CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGTCCTTATCTCACCTTCCTTAA	1333	
QY	481	ACTAAAGGTTCTTTACAGGCTTAATGTAAAGCATGCGCATTTCTTATCAGGTGGTCTT	540	
DB	1332	ACTAAAGGTTCTTTACAGGCTTAATGTAAAGCATGCGCATTTCTTATCAGGTGGTCTT	1273	
QY	541	GAGCTGCAGATACAAATCAGATCGTTTCATGGTGATCCAACCTGGATGTCAACTAGAGCCATG	600	

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Db 1272 GAGCTGCAGATACAATCGCATCGTTTCATGTGTGATCCAACTGGATGTCAACTAGAGCCATG 1213
|||||
Qy 601 GTCTTAGCTCTACCCCTCCCTTGTGATGTGCCAGGCTCAAACCTGTAATACCT 652
|||||
Db 1212 GTCTTAGCTCTACCCCTCCCTTGTGATGTGCCAGGCTCAAACCTGTAATACCT 1161
|||||

RESULT 7
US-10-260-539-7/c
; Sequence 7, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)..(1288)
; OTHER INFORMATION:
US-10-260-539-7

```

Query Match.	2.0%;	Score 601;	DB 9;	Length 2253;
Best Local Similarity	99.8%;	Pred. No. 2e-262;		
Matches 651;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;				
QY	1	GTATATGTAAGAAGCCTCATCTTTTGATTGTTTTAAATATACAAGATCGTTTCTTTAAGAGA	60	
Db	1812	GTATATGTAGAAGCCTCATCTTTTGATTGTTTTAAATATACAAGATCGTTTCTTTAAGAGA	1753	
QY	61	GCAAGATTCAAAATTTGTTTGCTGTTTCAAAATTTAAAAATTAATTTATCTCCTAAATTTT	120	
Db	1752	GCAAGATTCAAAATTTGTTTGCTGTTTCAAAATTTAAAAATTAATTTATCTCCTAAATTTT	1693	
QY	121	CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT	180	
Db	1692	CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT	1633	
QY	181	AACTCAACATATGTAAAGCTCTGGTGTACCTGGTGTATATATACCAAAAAAACAATTTGAT	240	
Db	1632	AACTCAACATATGTAAAGCTCTGGTGTACCTGGTGTATATATACCAAAAAAACAATTTGAT	1573	

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QY 241 CTATATACACATAGACATGAATATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 300
Db 1572 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 1513
QY 301 ACTATTATTAAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 360
Db 1512 ACTATTATTAAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 1453
QY 361 TTGCCATGGCATTAAACAAAGAGGCTGAGACTCAGCAACCCTTTGTGTTCAATTCGATTTG 420
Db 1452 TTGCCATGGCATTAAACAAAGAGGCTGAGACTCAGCAACCCTTTGTGTTCAATTCGATTTG 1393
QY 421 CAGGCTAGTAGTAAGTTTGGTGTCTGTAGTAAAGGCTCTTTATCTACCCCTCCTTAA 480
Db 1392 CAGGCTAGTAGTAAGTTTGGTGTCTGTAGTAAAGGCTCTTTATCTACCCCTCCTTAA 1333
QY 481 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGTCCTT 540
Db 1332 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGTCCTT 1273
QY 541 GAGCTGCAGATACAAATCGATCGTTTCATGTGTGATCCAACTGGATGTCAACTAGAGCCATG 600
Db 1272 GAGCTGCAGATACAAATCGATCGTTTCATGTGTGATCCAACTGGATGTCAACTAGAGCCATG 1213
QY 601 GTCTTAGCTACCCCTCCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652
Db 1212 GTCTTAGCTACCCCTCCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1161
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RESULT 8

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US-09-915-582-17/c
; Sequence 17, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3798
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-915-582-17
```

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Query Match 2.0%; Score 601; DB 10; Length 3798;
Best Local Similarity 99.8%; Pred. No. 2.le-262;
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAAGAGGCTCATCTTTTGAATTTTAAATATACAAGATGCTTTCTTTAAAGAGA 60
Db 1802 GTATATGTAAAGAGGCTCATCTTTTGAATTTTAAATATACAAGATGCTTTCTTTAAAGAGA 1743
QY 61 GCAAGATTCAAAATGTTTTGTCTTCAAAATTTAAATTTATCTCCTAAATTTT 120
Db 1742 GCAAGATTCAAAATGTTTTGTCTTCAAAATTTAAATTTATCTCCTAAATTTT 1683
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 180
Db 1682 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 1623
QY 181 AACTCAACATATGTAGCTCTGGTGTACCTGCTTATATATACCAAAAAAACAATTGAT 240
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Db 1622 AACTCAACATATGTAGCTCTGGTGTACCTGCTTATATATACCAAAAAAACAATTGAT 1563
QY 241 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 300
Db 1562 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 1503
QY 301 ACTATTATTAAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 360
Db 1502 ACTATTATTAAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 1443
QY 361 TTGCCATGGCATTAAACAAAGAGGCTGAGACTCAGCAACCCTTTGTGTTCAATTCGATTTG 420
Db 1442 TTGCCATGGCATTAAACAAAGAGGCTGAGACTCAGCAACCCTTTGTGTTCAATTCGATTTG 1383
QY 421 CAGGCTAGTAGTAAGTTTGGTGTCTGTAGTAAAGGCTCTTTATCTACCCCTCCTTAA 480
Db 1382 CAGGCTAGTAGTAAGTTTGGTGTCTGTAGTAAAGGCTCTTTATCTACCCCTCCTTAA 1323
QY 481 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGTCCTT 540
Db 1322 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGTCCTT 1263
QY 541 GAGCTGCAGATACAAATCGATCGTTTCATGTGTGATCCAACTGGATGTCAACTAGAGCCATG 600
Db 1262 GAGCTGCAGATACAAATCGATCGTTTCATGTGTGATCCAACTGGATGTCAACTAGAGCCATG 1203
QY 601 GTCTTAGCTACCCCTCCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652
Db 1202 GTCTTAGCTACCCCTCCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1151
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RESULT 9

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US-09-915-582-35/c
; Sequence 35, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 4001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-915-582-35
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Query Match 2.0%; Score 601; DB 10; Length 4001;
Best Local Similarity 99.8%; Pred. No. 2.le-262;
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAAGAGGCTCATCTTTTGAATTTTAAATATACAAGATGCTTTCTTTAAAGAGA 60
Db 1999 GTATATGTAAAGAGGCTCATCTTTTGAATTTTAAATATACAAGATGCTTTCTTTAAAGAGA 1940
QY 61 GCAAGATTCAAAATGTTTTGTGTTTCAAAATTTAAATTTATCTCCTAAATTTT 120
Db 1939 GCAAGATTCAAAATGTTTTGTGTTTCAAAATTTAAATTTATCTCCTAAATTTT 1880
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 180
Db 1879 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 1820
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Qy	585	GTCACTAGAGCCATGGTCTTTAGCTTACCCCTCCCTCTTGATGTGGCCAGGCTCAAAC	644
Db	1278	GTCACTAGAGCCATGGTCTTTAGCTTACCCCTCCCTCTTGATGTGGCCAGGCTCAAAC	1219
Qy	645	TAATACCT	652
Db	1218	TAATACCT	1211

RESULT 14

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US-10-226-559-1/c
; Sequence 1, Application US/10226559
; Publication No. US20030105015A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/10/226,559
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-10-226-559-1

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Search completed: July 8, 2003, 19:41:40
Job time : 3100 secs